theAwesome_EnsModel

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1 Ensemble Model

- **Course**: Data Mining
- **Team Name**: The Awesome
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1.1 Step 0: Data Preparation and Cleaning

```
In [72]: import pandas as pd
         import matplotlib.pyplot as plt
```

```
In [73]: # Read CSV data into df
         df = pd.read_csv('./theAwesome_EnsModel.csv')
         # delete id column no need
         df.drop('Id',axis=1,inplace=True)
         df.head()
```

```
Out[73]:    SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm      Species
         0            5.1           3.5            1.4           0.2  Iris-setosa
         1            4.9           3.0            1.4           0.2  Iris-setosa
         2            4.7           3.2            1.3           0.2  Iris-setosa
         3            4.6           3.1            1.5           0.2  Iris-setosa
         4            5.0           3.6            1.4           0.2  Iris-setosa
```

```
In [74]: # Learn the unique values in diagnosis column
         print("Classification labels: ", df.Species.unique() )
```

```
Classification labels:  ['Iris-setosa' 'Iris-versicolor' 'Iris-virginica']
```

```
In [75]: # Mapping labels to numerical labels?
         df.Species = df.Species.map({'Iris-setosa':0, 'Iris-versicolor':1, 'Iris-virginica':2})
```

Generate the information about your dataset: number of columns and rows, names and data types of the columns, memory usage of the dataset.

Hint: Pandas data frame info() function.

Generate descriptive statistics of all columns (input and output) of your dataset. Descriptive statistics for numerical columns include: count, mean, std, min, 25 percentile (Q1), 50 percentile (Q2, median), 75 percentile (Q3), max values of the columns. For categorical columns, determine distinct values and their frequency in each categorical column.

Hint: Pandas, data frame describe() function.

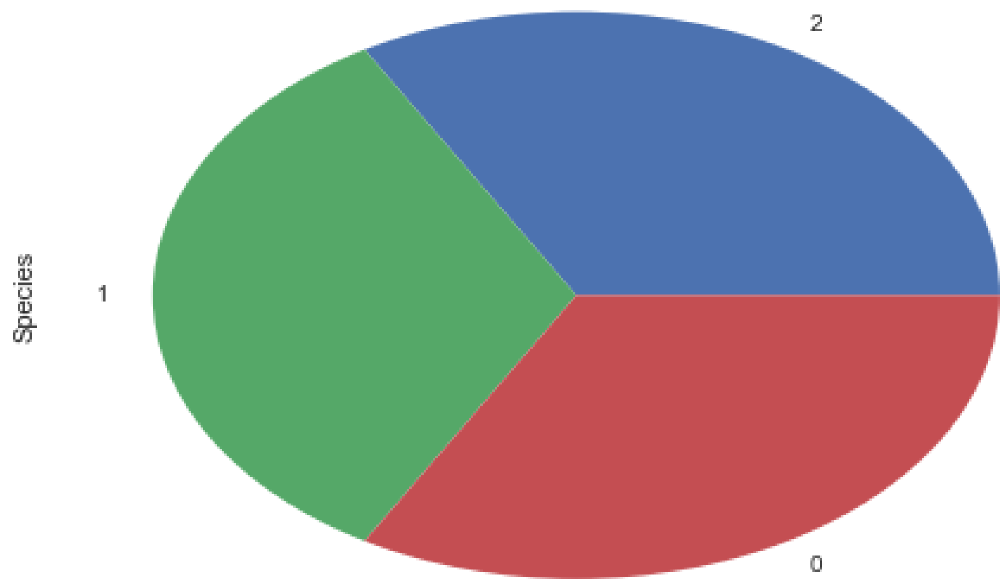
```
In [76]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
SepalLengthCm    150 non-null float64
SepalWidthCm     150 non-null float64
PetalLengthCm    150 non-null float64
PetalWidthCm     150 non-null float64
Species          150 non-null int64
dtypes: float64(4), int64(1)
memory usage: 5.9 KB
```

```
In [77]: df.describe()
```

```
Out[77]:        SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm     Species
         count     150.000000    150.000000     150.000000    150.000000  150.000000
         mean        5.843333      3.054000       3.758667      1.198667    1.000000
         std         0.828066      0.433594       1.764420      0.763161    0.819232
         min         4.300000      2.000000       1.000000      0.100000    0.000000
         25%         5.100000      2.800000       1.600000      0.300000    0.000000
         50%         5.800000      3.000000       4.350000      1.300000    1.000000
         75%         6.400000      3.300000       5.100000      1.800000    2.000000
         max         7.900000      4.400000       6.900000      2.500000    2.000000
```

```
In [78]: df.Species.value_counts().plot(kind='pie')
         plt.show()
```



Split your data into Training and Test data set by randomly selecting; use 70% for training and 30 % for testing. Generate descriptive statistics of all columns (input and output) of Training and Test datasets. Review the descriptive statistics of input output columns in Train, Test and original Full (before the splitting operation) datasets and compare them to each other. Are they similar or not? Do you think Train and Test dataset are representative of the Full datasets ? why ?

Hint: Scikit learn, data train_test_split(), stratified function.

```
In [79]: df.Species.value_counts(df.Species.unique()[0])
```

```
Out[79]: 2    50
         1    50
         0    50
         Name: Species, dtype: int64
```

```
In [80]: # Splitting train and test data
         # .7 and .3
         import numpy as np
         msk = np.random.rand(len(df)) < 0.7
         train_df = df[msk]
         test_df = df[~msk]
```

```
In [81]: train_df.describe()
```

```
Out[81]:        SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm    Species
         count      98.000000     98.000000      98.000000     98.000000  98.000000
         mean         5.739796      3.045918       3.593878      1.141837   0.938776
         std          0.828580      0.431532       1.781799      0.774453   0.835011
         min          4.300000      2.000000       1.100000      0.100000   0.000000
         25%          5.000000      2.800000       1.500000      0.300000   0.000000
         50%          5.700000      3.000000       4.150000      1.300000   1.000000
         75%          6.300000      3.375000       5.100000      1.800000   2.000000
         max          7.700000      4.400000       6.900000      2.500000   2.000000
```

```
In [82]: test_df.describe()
```

```
Out[82]:        SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm    Species
         count      52.000000     52.000000      52.000000     52.000000  52.000000
         mean        6.038462      3.069231       4.069231      1.305769   1.115385
         std         0.798811      0.441272       1.704842      0.736822   0.783503
         min         4.600000      2.200000       1.000000      0.100000   0.000000
         25%         5.475000      2.875000       2.875000      0.850000   0.750000
         50%         6.100000      3.000000       4.600000      1.400000   1.000000
         75%         6.500000      3.300000       5.250000      1.800000   2.000000
         max         7.900000      4.100000       6.600000      2.500000   2.000000
```

```
In [83]: df.describe()
```

```
Out[83]:        SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm     Species
         count     150.000000    150.000000     150.000000    150.000000  150.000000
         mean        5.843333      3.054000       3.758667      1.198667    1.000000
         std         0.828066      0.433594       1.764420      0.763161    0.819232
         min         4.300000      2.000000       1.000000      0.100000    0.000000
         25%         5.100000      2.800000       1.600000      0.300000    0.000000
         50%         5.800000      3.000000       4.350000      1.300000    1.000000
         75%         6.400000      3.300000       5.100000      1.800000    2.000000
         max         7.900000      4.400000       6.900000      2.500000    2.000000
```

They are pretty similar to full data when I print the descriptive stats for test and train data.

1.2 Step 3: Analysis of the Output Column

Analyze the output columns in Train and Test dataset. If the output column is numerical then calculate the IQR (inter quartile range, Q3-Q1) and Range (difference between max and min value). If your output column is categorical then determine if the column is nominal or ordinal, why?. Is there a class imbalance problem? (check if there is big difference between the number of distinct values in your categorical output column)

```
In [84]: print(train_df["Species"].value_counts(train_df["Species"].unique()[0]))
         print(len(train_df))
         train_df.head()
```

```
0    37
2    31
1    30
Name: Species, dtype: int64
98
```

```
Out[84]:    SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm  Species
         1            4.9           3.0            1.4           0.2        0
         2            4.7           3.2            1.3           0.2        0
         3            4.6           3.1            1.5           0.2        0
         4            5.0           3.6            1.4           0.2        0
         5            5.4           3.9            1.7           0.4        0
```

```
In [85]: print(test_df["Species"].value_counts(test_df["Species"].unique()[0]))
         print(len(test_df))
         test_df.head()
```

```
1    20
2    19
0    13
Name: Species, dtype: int64
52
```

```
Out[85]:     SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm  Species
         0             5.1           3.5            1.4           0.2        0
         14            5.8           4.0            1.2           0.2        0
         16            5.4           3.9            1.3           0.4        0
         19            5.1           3.8            1.5           0.3        0
         22            4.6           3.6            1.0           0.2        0
```

My target/label column is nominal categorical data. This data will be used for multi-class classification. When I am splitting the test and train data, I was careful to get the similar ratio of the labels for each...

1.3 Step 4: Scale Training and Test dataset

Using one of the scaling method (max, min-max, standard or robust), create a scaler object and scale the numerical input columns of the Training dataset. Using the same scaler object, scale the numerical input columns of the Test set. Generate the descriptive statistics of the scaled input columns of Training and Test set. If some of the input columns are categorical then convert them to binary columns using one-hotencoder() function (scikit learn) or dummy() function (Pandas data frame).

Hint: - http://scikit-learn.org/stable/modules/preprocessing.html#preprocessing

```
In [86]: # I am going to apply min-max scaling for my data.
         from sklearn import preprocessing
         # Fitting the minmax scaled version for training data
         minmax_scale = preprocessing.MinMaxScaler().fit(train_df.iloc[:, :4])
         # Now actually scale train and test data
         train_df.iloc[:, :4] = minmax_scale.transform(train_df.iloc[:, :4])
         test_df.iloc[:, :4] = minmax_scale.transform(test_df.iloc[:, :4])
```

```
/Users/eneskemalergin/anaconda3/lib/python3.5/site-packages/pandas/core/indexing.py:477: Setting
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html#
  self.obj[item] = s
```

```
In [87]: train_df.describe()
```

```
Out[87]:        SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm    Species
         count      98.000000     98.000000      98.000000     98.000000  98.000000
         mean        0.423469      0.435799       0.429979      0.434099   0.938776
         std         0.243700      0.179805       0.307207      0.322689   0.835011
         min         0.000000      0.000000       0.000000      0.000000   0.000000
         25%         0.205882      0.333333       0.068966      0.083333   0.000000
         50%         0.411765      0.416667       0.525862      0.500000   1.000000
         75%         0.588235      0.572917       0.689655      0.708333   2.000000
         max         1.000000      1.000000       1.000000      1.000000   2.000000
```

```
In [88]: test_df.describe()
```

```
Out[88]:        SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm    Species
         count      52.000000     52.000000      52.000000     52.000000  52.000000
         mean        0.511312      0.445513       0.511936      0.502404   1.115385
         std         0.234945      0.183863       0.293938      0.307009   0.783503
         min         0.088235      0.083333      -0.017241      0.000000   0.000000
         25%         0.345588      0.364583       0.306034      0.312500   0.750000
         50%         0.529412      0.416667       0.603448      0.541667   1.000000
         75%         0.647059      0.541667       0.715517      0.708333   2.000000
         max         1.058824      0.875000       0.948276      1.000000   2.000000
```

```
In [89]: # Input and Output
         inp_train = train_df.iloc[:, :4]
         out_train = train_df["Species"]
         inp_test = test_df.iloc[:, :4]
         out_test = test_df["Species"]
```

Using one of the methods (Gradient Boosting Machines, Random Forest) build your ensemble predictive model using the scaled input columns of Training set. To find the optimum values for the model parameters, use Grid Search with k-fold cross-validation in building your model. Grid Search is one of the method used to perform Hyper Parameter optimization to generate more accurate (better generalized) models.

Hint: - http://scikit-learn.org/stable/supervised_learning.html#supervised-learning - http://scikit-learn.org/stable/modules/cross_validation.html - http://scikit-learn.org/stable/modules/generated/sklearn.model_selection.GridSearchCV.html - http://scikit-learn.org/stable/modules/grid_search.html - http://scikit-learn.org/stable/modules/ensemble.html#random-forests - http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.GradientBoostingClassifier.html - http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.GradientBoostingRegressor.html

```
In [90]: from sklearn.cross_validation import cross_val_score
         from sklearn.ensemble import RandomForestClassifier
         from sklearn.model_selection import GridSearchCV

         # Building a RandomForest with 10 estimators
         clf = RandomForestClassifier(n_estimators=10)

         # clf = clf.fit(inp_train, out_train)
         # 10-fold Cross validation
         print("Average of 10 cross validation: ", np.mean(cross_val_score(clf, inp_train, out_t
```

```
Average of 10 cross validation:  0.97
```

```
In [91]: param_grid = {
                          'n_estimators': [5, 10, 15, 20],
                          'max_depth': [2, 5, 7, 9]
                      }
         grid_clf = GridSearchCV(clf, param_grid, cv=10)
         grid_clf.fit(inp_train, out_train)
         print(grid_clf)
```

```
GridSearchCV(cv=10, error_score='raise',
       estimator=RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gini',
            max_depth=None, max_features='auto', max_leaf_nodes=None,
            min_impurity_split=1e-07, min_samples_leaf=1,
            min_samples_split=2, min_weight_fraction_leaf=0.0,
            n_estimators=10, n_jobs=1, oob_score=False, random_state=None,
            verbose=0, warm_start=False),
       fit_params={}, iid=True, n_jobs=1,
       param_grid={'max_depth': [2, 5, 7, 9], 'n_estimators': [5, 10, 15, 20]},
       pre_dispatch='2*n_jobs', refit=True, return_train_score=True,
       scoring=None, verbose=0)
```

```
In [92]: print(grid_clf.best_estimator_)
```

```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gini',
            max_depth=5, max_features='auto', max_leaf_nodes=None,
            min_impurity_split=1e-07, min_samples_leaf=1,
            min_samples_split=2, min_weight_fraction_leaf=0.0,
            n_estimators=5, n_jobs=1, oob_score=False, random_state=None,
            verbose=0, warm_start=False)
```

```
In [93]: print(grid_clf.best_params_)
```

```
{'max_depth': 5, 'n_estimators': 5}
```

```
In [94]: print(grid_clf.best_score_)
```

```
0.969387755102
```

```
In [95]: # Using optimized parameterss to train my data
         # Optimized parameters:
         clf = RandomForestClassifier(max_depth=5, n_estimators=5, random_state=None)
         clf.fit(inp_train, out_train)
         print("Average of 10 cross validation of optimized estimetor: ",
               np.mean(cross_val_score(clf, inp_train, out_train, cv=5)))
```

```
Average of 10 cross validation of optimized estimetor:  0.948370927318
```

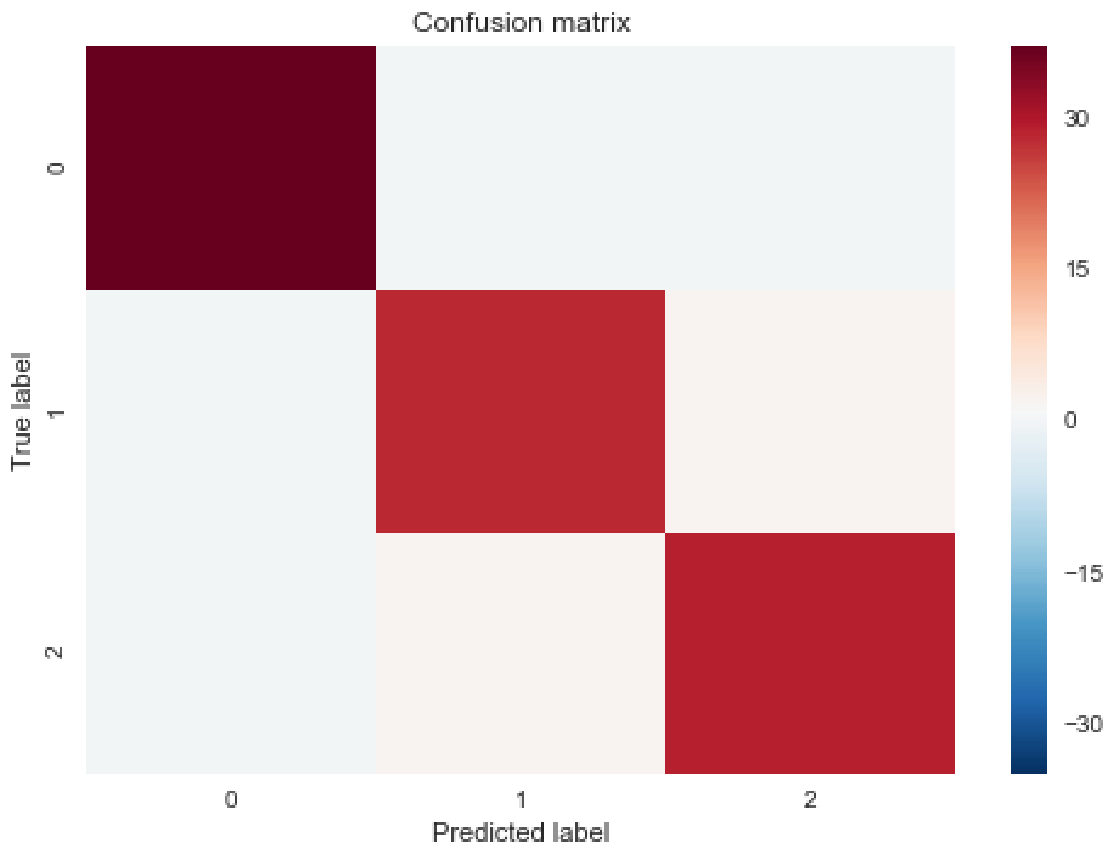
Apply your model to input (scaled) columns of Training dataset to obtain the predicted output for Training dataset. If your model is regression then plot actual output versus predicted output column of Training dataset. If your model is classification then generate confusion matrix on actual and predicted columns of Training dataset.

Hint: Matplotlip, Seaborn, Bokeh scatter(), plot() functions - http://scikit-learn.org/0.15/auto_examples/plot_confusion_matrix.html - http://scikit-learn.org/stable/auto_examples/model_selection/plot_confusion_matrix.html

```
In [96]: # importing libraries for plotting
         # Importing library for confusion matrix
         from sklearn.metrics import confusion_matrix
         import matplotlib.pyplot as plt
         import seaborn as sns
         import itertools
         sns.set(style='darkgrid')
```

```
In [97]: # train prediction for train data
         out_train_pred = clf.predict(inp_train)
         # Compute confusion matrix for prediction of train
         cm = confusion_matrix(out_train, out_train_pred)
         print(cm)

         sns.heatmap(cm, center=True)
         plt.title('Confusion matrix')
         plt.ylabel('True label')
         plt.xlabel('Predicted label')
         plt.show()
```

```
[[37  0  0]
 [ 0 28  2]
 [ 0  2 29]]
```



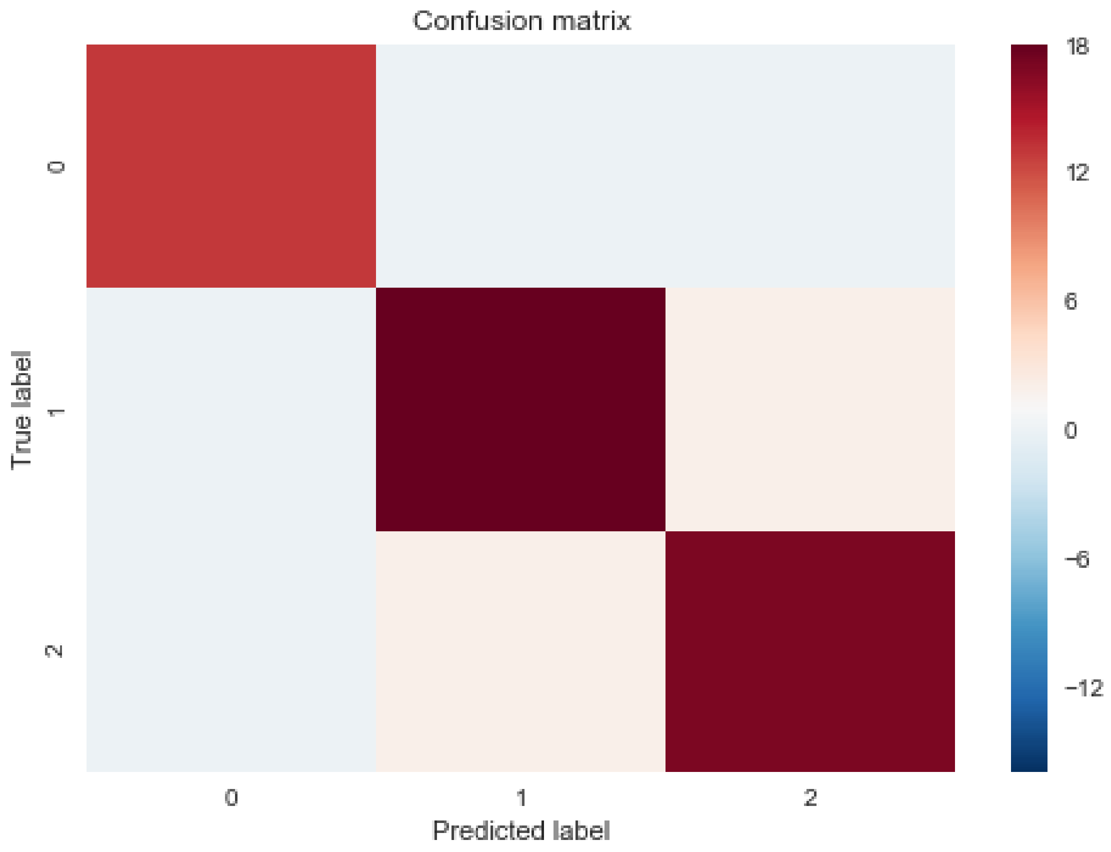
Apply your model to input (scaled) columns of Test dataset to obtain the predicted output for Test dataset. If your model is regression then plot actual output versus predicted output column of Test dataset. If your model is classification then generate confusion matrix on actual and predicted columns of Test dataset.

> Hint: Matplotlip, Seaborn, Bokeh scatter(), plot() functions - http://scikit-learn.org/0.15/auto_examples/plot_confusion_matrix.html - http://scikit-learn.org/stable/auto_examples/model_selection/plot_confusion_matrix.html

```
In [98]: # test prediction for test data
         out_test_pred = clf.predict(inp_test)
         # Compute confusion matrix for prediction of train
         cm = confusion_matrix(out_test, out_test_pred)
         print(cm)

         sns.heatmap(cm, center=True)
```

```
        plt.title('Confusion matrix')
        plt.ylabel('True label')
        plt.xlabel('Predicted label')
        plt.show()
```

```
[[13  0  0]
 [ 0 18  2]
 [ 0  2 17]]
```

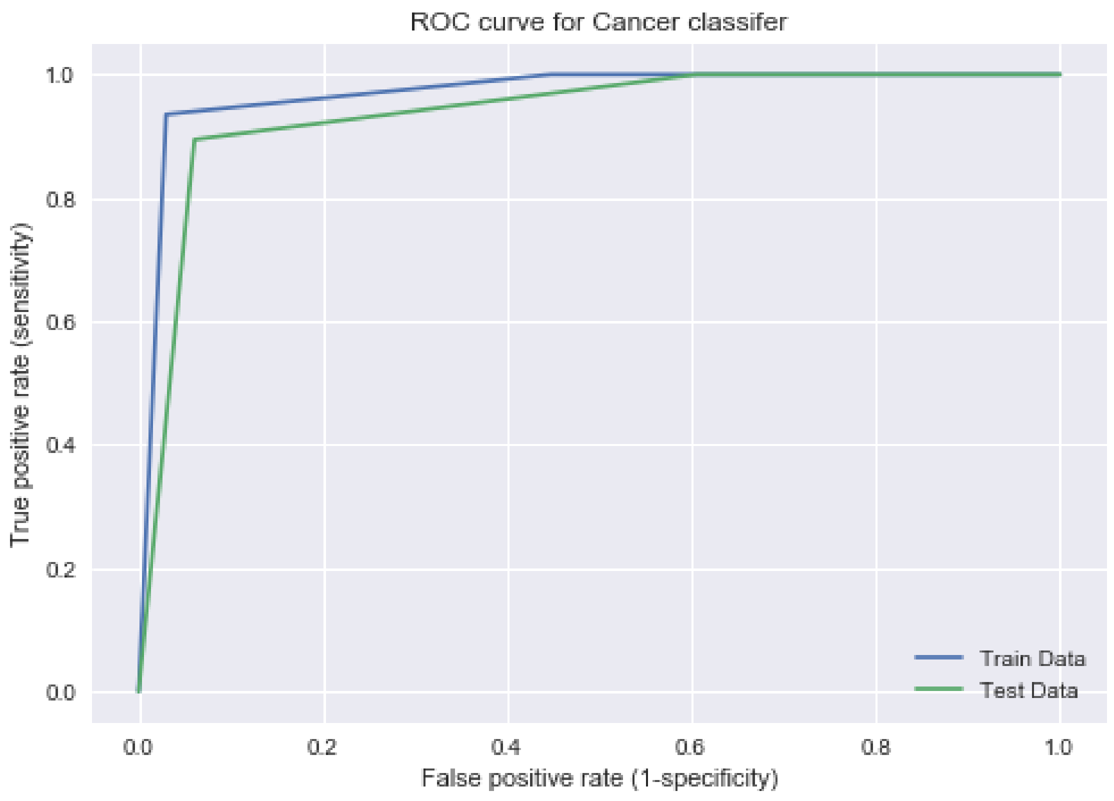


Using one of the error (evaluation) metrics (classification or regression), calculate the performance of the model on Training set and Test set. Compare the performance of the model on Training and Test set. Which one (Training or Testing performance) is better, is there an overfitting case, why ?. Would you deploy (Productionize) this model for using in your business system? why ?

Classification Metrics: Accuracy, Precision, Recall, F-score, Recall, AUC, ROC etc Regression Metrics: RMSE, MSE, MAE, R2 etc

Hint: - http://scikit-learn.org/stable/model_selection.html#model-selection - http://scikit-learn.org/stable/modules/model_evaluation.html#classification-report

```
In [99]: # I would like to use ROC
         # Area under ROC Curve (or AUC for short) is
         #  a performance metric for binary classification problems.
         from sklearn.metrics import roc_curve
         # ROC curve for train data
         fpr,tpr,thresholds = roc_curve(out_train, out_train_pred,pos_label=2)
         # plot the curve
         plt.plot(fpr, tpr, label="Train Data")
         # ROC curve for test data
         fpr, tpr, thresholds = roc_curve(out_test, out_test_pred, pos_label=2)
         # Plotting the curves
         plt.plot(fpr, tpr, label="Test Data")
         plt.xlim([-0.05,1.05])
         plt.ylim([-0.05,1.05])
         plt.title('ROC curve for Cancer classifer')
         plt.xlabel('False positive rate (1-specificity)')
         plt.ylabel('True positive rate (sensitivity)')
         plt.legend(loc=4,)
         plt.show()
```



Train data is performing slightly better than the test data however, I believe it is overfitting, as you can see in the Train data ROC curve, it started very high and hit 1.0 sooner.

This model is not yet deployable because I did not check other models and tweaking the parameters.

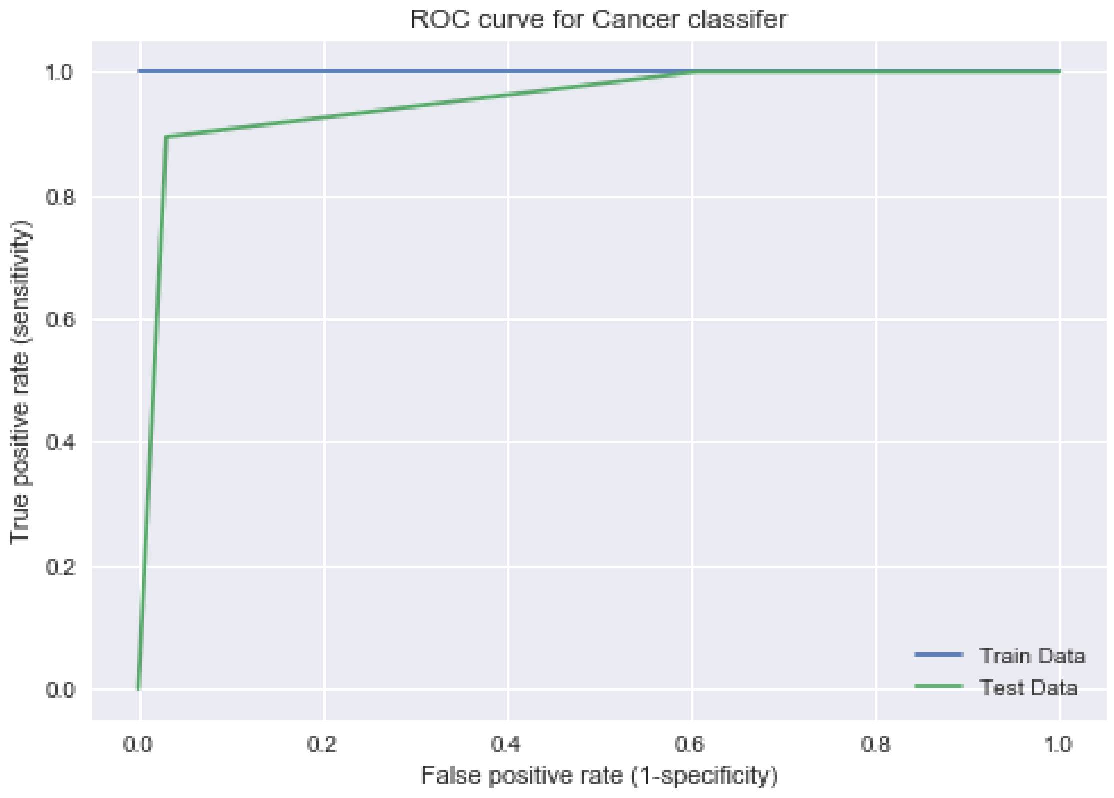
1.4 Step 9: Update the Model

Go back to Step5, and choose random values (use default values) of the model parameters and re-train the model. Repeat Steps: 6, 7 and 8. Using the same error metric, generate the accuracy of the model on Training and Test dataset. Did you get a better or worse performance on Training or Test set? Explain why the new model performs better or worse than the former model. What does hyperparameter optimization (grid search) on model building enable?

```
In [100]: # Using default values for RandomForeset Classifier
          # Building a RandomForest
          clf = RandomForestClassifier()

          clf = clf.fit(inp_train, out_train)

In [101]: # train prediction for train data
          out_train_pred = clf.predict(inp_train)
          # Compute confusion matrix for prediction of train
          cm = confusion_matrix(out_train, out_train_pred)
          print(cm)

          # test prediction for test data
          out_test_pred = clf.predict(inp_test)
          # Compute confusion matrix for prediction of train
          cm = confusion_matrix(out_test, out_test_pred)
          print(cm)
```

```
[[37  0  0]
 [ 0 30  0]
 [ 0  0 31]]
[[13  0  0]
 [ 0 19  1]
 [ 0  2 17]]
```

```
In [102]: # Model trained with default values
          # ROC curve for train data
          fpr,tpr,thresholds = roc_curve(out_train, out_train_pred,pos_label=2)
          # plot the curve
          plt.plot(fpr, tpr, label="Train Data")
          # ROC curve for test data
          fpr, tpr, thresholds = roc_curve(out_test, out_test_pred, pos_label=2)
          # Plotting the curves
          plt.plot(fpr, tpr, label="Test Data")
          plt.xlim([-0.05,1.05])
plt.ylim([-0.05,1.05])
plt.title('ROC curve for Cancer classifer')
plt.xlabel('False positive rate (1-specificity)')
plt.ylabel('True positive rate (sensitivity)')
plt.legend(loc=4,)
plt.show()
```



As you can see from the graph train data is clearly overfitted, which means random forest with default parameters did not work for this dataset. Test data is still learning well but model is not really working with default parameters.

1.5 Step 10: Change the Error Metric

Choose another error metric other than you used in Step 8 and evaluate the performance of the model (optimized) on Training and Test dataset by generating the accuracy of the model based on the new metric. Compare the results and explain which error metric is better for your modeling and why?

```
In [103]: # Let's check f1 score on our classification
          from sklearn.metrics import f1_score
          print("f1_score: ", f1_score(out_test, out_test_pred, average=None))
```

```
f1_score:  [ 1.          0.92682927  0.91891892]
```

I personally prefer ROC curve for more visual allowance when it comes to measuring error/accuracy. But f1 score is showing the error of each class in very simplistic way.