S4 - HOPE random forest

December 6, 2020

1 Import data from DB.

[1]:
```
import pandas as pd
import numpy as np
```

[2]:
```
dfOrg = pd.read_csv('hope_dataset_cleaned.csv')

print(dfOrg.shape[0])
```

```
1243
```

[3]:
```
dfOrg.head(10)
```

[3]:

	pedido.data.attributes.age	pedido.data.attributes.diagnostic_main	pedido.data.attributes.gender	articulo	respuesta.articlesRevisedYear
0	75.0	FISTULA PERITONEAL	male	27395425	2018
1	75.0	FISTULA PERITONEAL	male	28560554	2018
2	75.0	FISTULA PERITONEAL	male	28641726	2017
3	75.0	FISTULA PERITONEAL	male	26245344	2016
4	75.0	FISTULA PERITONEAL	male	28942543	2018
5	75.0	FISTULA PERITONEAL	male	24782153	2014
6	75.0	FISTULA PERITONEAL	male	28002229	2018
7	75.0	FISTULA PERITONEAL	male	27505109	2017
8	75.0	FISTULA PERITONEAL	male	24850546	2015
9	75.0	FISTULA PERITONEAL	male	29371050	2019

```
   respuesta.articlesRevisedMonth  \
0                               1
1                               4
2                              12
3                              12
4                               6
5                               6
6                               9
7                               4
8                               1
9                               4

                              respuesta.pubmed_keys  utilidad
0  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       1.0
1  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
2  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
3  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
4  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
5  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
6  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
7  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
8  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
9  Abdomen,Adenocarcinoma,Antiemetics,Blood Cultu…       NaN
```

2 Transform (factorice) from Categories to continuous atributes

Transform 'pedido.data.attributes.diagnostic_main' atribute

[4]:
```
dataDiagnosticMain, categoriesDiagnosticMain = pd.factorize(dfOrg['pedido.data.
↪attributes.diagnostic_main'])

dfOrg['pedido.data.attributes.diagnostic_main'] = dataDiagnosticMain
```

Transform 'gender' atribute

[5]:
```
dataGender, categoriesGender = pd.factorize(dfOrg['pedido.data.attributes.
↪gender'])

dfOrg['pedido.data.attributes.gender'] = dataGender
```

Transform 'respuesta.pubmed_keys' atribute

[6]:
```
categoriesORGPubMedKeys = dfOrg['respuesta.pubmed_keys'].value_counts()

print("total: " + str(categoriesORGPubMedKeys.size))
```

```
total: 80
```

[7]:
```
dataPubMedKeys, categoriesPubMedKeys = pd.factorize(dfOrg['respuesta.
↪pubmed_keys'])

dfOrg['respuesta.pubmed_keys'] = dataPubMedKeys
```

[8]:
```
dfOrg.head(10)
```

[8]:

	pedido.data.attributes.age	pedido.data.attributes.diagnostic_main	\
0	75.0	0	
1	75.0	0	
2	75.0	0	
3	75.0	0	
4	75.0	0	
5	75.0	0	
6	75.0	0	
7	75.0	0	
8	75.0	0	
9	75.0	0	

	pedido.data.attributes.gender	articulo	respuesta.articlesRevisedYear	\
0	0	27395425	2018	
1	0	28560554	2018	
2	0	28641726	2017	
3	0	26245344	2016	
4	0	28942543	2018	
5	0	24782153	2014	
6	0	28002229	2018	
7	0	27505109	2017	
8	0	24850546	2015	
9	0	29371050	2019	

	respuesta.articlesRevisedMonth	respuesta.pubmed_keys	utilidad
0	1	0	1.0
1	4	0	NaN
2	12	0	NaN
3	12	0	NaN
4	6	0	NaN
5	6	0	NaN
6	9	0	NaN
7	4	0	NaN
8	1	0	NaN
9	4	0	NaN

[9]:
```
print("age NaN => " + str(dfOrg[pd.isnull(dfOrg['pedido.data.attributes.age'])].
↪shape[0]))
print("diagnostic_main NaN => " + str(dfOrg[pd.isnull(dfOrg['pedido.data.
↪attributes.diagnostic_main'])].shape[0]))
```

```
print("gender NaN => " + str(dfOrg[pd.isnull(dfOrg['pedido.data.attributes.
 ↪gender'])].shape[0]))
print("articulo NaN => " + str(dfOrg[pd.isnull(dfOrg['articulo'])].shape[0]))
print("articlesRevisedYear NaN => " + str(dfOrg[pd.isnull(dfOrg['respuesta.
 ↪articlesRevisedYear'])].shape[0]))
print("articlesRevisedMonth NaN => " + str(dfOrg[pd.isnull(dfOrg['respuesta.
 ↪articlesRevisedMonth'])].shape[0]))
print("pubmed_keys NaN => " + str(dfOrg[pd.isnull(dfOrg['respuesta.
 ↪pubmed_keys'])].shape[0]))
print("utilidad NaN => " + str(dfOrg[pd.isnull(dfOrg['utilidad'])].shape[0]))
```

```
age NaN => 10
diagnostic_main NaN => 0
gender NaN => 0
articulo NaN => 0
articlesRevisedYear NaN => 0
articlesRevisedMonth NaN => 0
pubmed_keys NaN => 0
utilidad NaN => 1192
```

Remove row with age eq NaN

[10]:
```
dfOrg = dfOrg[pd.notnull(dfOrg['pedido.data.attributes.age'])]
```

3 Standardize the Data

Choosed “age”, “diagnostic_main”, “year”, “pubmed_keys” and “articulo” attributes (based on PCA_V2 study)

[11]:
```
from sklearn.preprocessing import StandardScaler

features = ["pedido.data.attributes.age",
    "pedido.data.attributes.diagnostic_main",
    "respuesta.articlesRevisedYear",
    "respuesta.pubmed_keys",
    "articulo"]

# Separating out the features
x = dfOrg.loc[:, features].values

featuresTransformed = StandardScaler().fit_transform(x)

dfStandarized = pd.DataFrame(featuresTransformed, index=dfOrg.index,␣
 ↪columns=features)
dfStandarized['utilidad'] = dfOrg['utilidad']

dfStandarized
```

[11]:

	pedido.data.attributes.age	pedido.data.attributes.diagnostic_main	\
0	1.443474	-1.360638	
1	1.443474	-1.360638	
2	1.443474	-1.360638	
3	1.443474	-1.360638	
4	1.443474	-1.360638	
…	…	…	
1238	-0.429381	-0.580827	
1239	-0.429381	-0.580827	
1240	-0.429381	-0.580827	
1241	-0.429381	-0.580827	
1242	-0.429381	-0.580827	

	respuesta.articlesRevisedYear	respuesta.pubmed_keys	articulo	utilidad
0	0.643671	-1.650220	-0.221939	1.0
1	0.643671	-1.650220	0.137839	NaN
2	0.224418	-1.650220	0.162904	NaN
3	-0.194835	-1.650220	-0.577070	NaN
4	0.643671	-1.650220	0.255793	NaN
…	…	…	…	…
1238	-0.194835	1.520816	0.574852	NaN
1239	1.062924	1.520816	-0.540973	NaN
1240	-0.614089	1.520816	0.801912	NaN
1241	1.062924	1.520816	-0.056202	NaN
1242	-0.614089	1.520816	-2.782199	NaN

[1233 rows x 6 columns]

4 Separe data by utilidad is defined

[12]:
```
dfDataSetComplete = dfStandarized[pd.notnull(dfStandarized['utilidad'])]

print(dfDataSetComplete.shape[0])

dfDataSetToPredict = dfStandarized[pd.isnull(dfStandarized['utilidad'])]

print(dfDataSetToPredict.shape[0])
```

```
51
1182
```

5 Random Forest

We check the number of results

[13]:
```
dfDataSetComplete.groupby('utilidad').size()
```

[13]:
```
utilidad
0.0    21
1.0    30
dtype: int64
```

Separe “utilidad” atribute from dataToTrain

[14]:
```
X = np.array(dfDataSetComplete.drop(['utilidad'],1))
y = np.array(dfDataSetComplete['utilidad'])
X.shape
```

[14]:
```
(51, 5)
```

[15]:
```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, random_state=0)
```

6 Exploring number of estimators

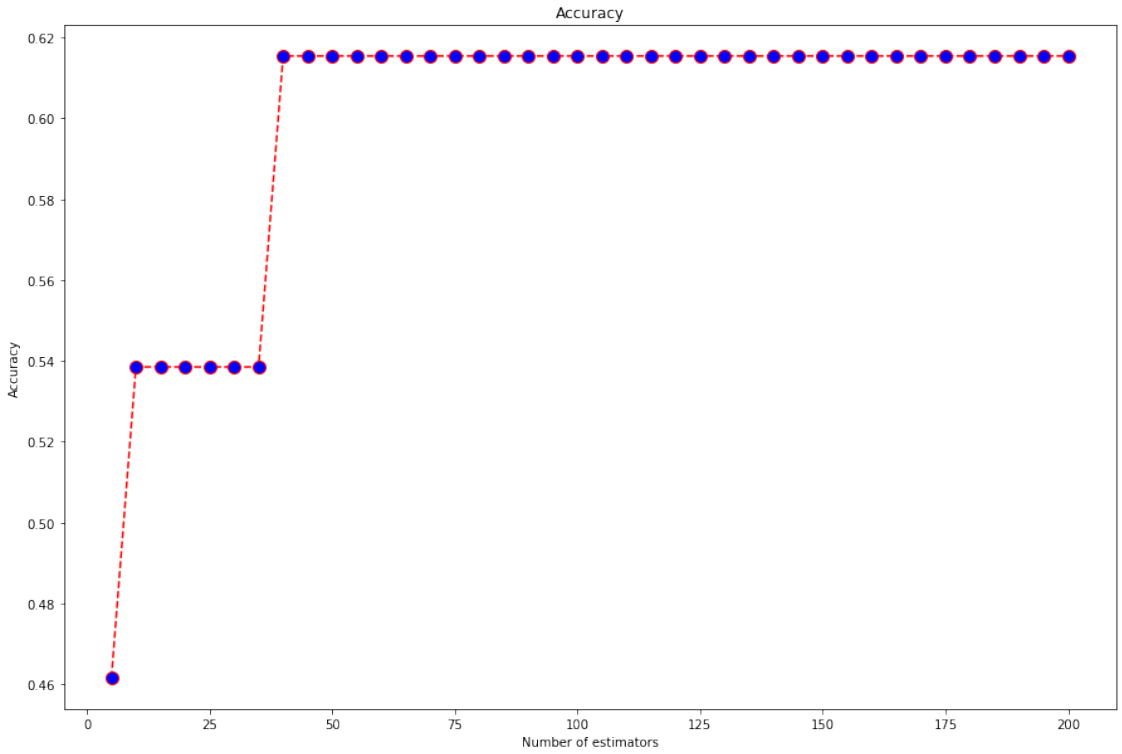
Via the sample size n of the bootstrap sample, we control the bias-variance tradeoff of the random forest. By choosing a larger value for n, we decrease the randomness and thus the forest is more likely to overfit. On the other hand, we can reduce the degree of overfitting by choosing smaller values for n at the expense of the model performance. In most implementations, including the RandomForestClassifier implementation in scikit-learn, the sample size of the bootstrap sample is chosen to be equal to the number of samples in the original training set, which usually provides a good bias-variance tradeoff.

https://towardsdatascience.com/gini-index-vs-information-entropy-7a7e4fed3fcb

[16]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix,␣
 ↪accuracy_score

k_range = range(5, 205, 5)
accuracy = []

for k in k_range:
    forest_test = RandomForestClassifier(
        criterion='entropy',
        n_estimators=k,
        random_state=0
    )
    forest_test.fit(X_train, y_train)
    y_pred_test = forest_test.predict(X_test)

    accuracy.append(accuracy_score(y_test, y_pred_test))
```

[17]:
```
import matplotlib.pyplot as plt

fig, axs = plt.subplots(figsize=(15, 10))
axs.plot(k_range, accuracy, color='red', linestyle='dashed', marker='o',
         markerfacecolor='blue', markersize=10)
axs.set_title('Accuracy')
axs.set_xlabel('Number of estimators')
axs.set_ylabel('Accuracy')
```

[17]:
```
Text(0, 0.5, 'Accuracy')
```



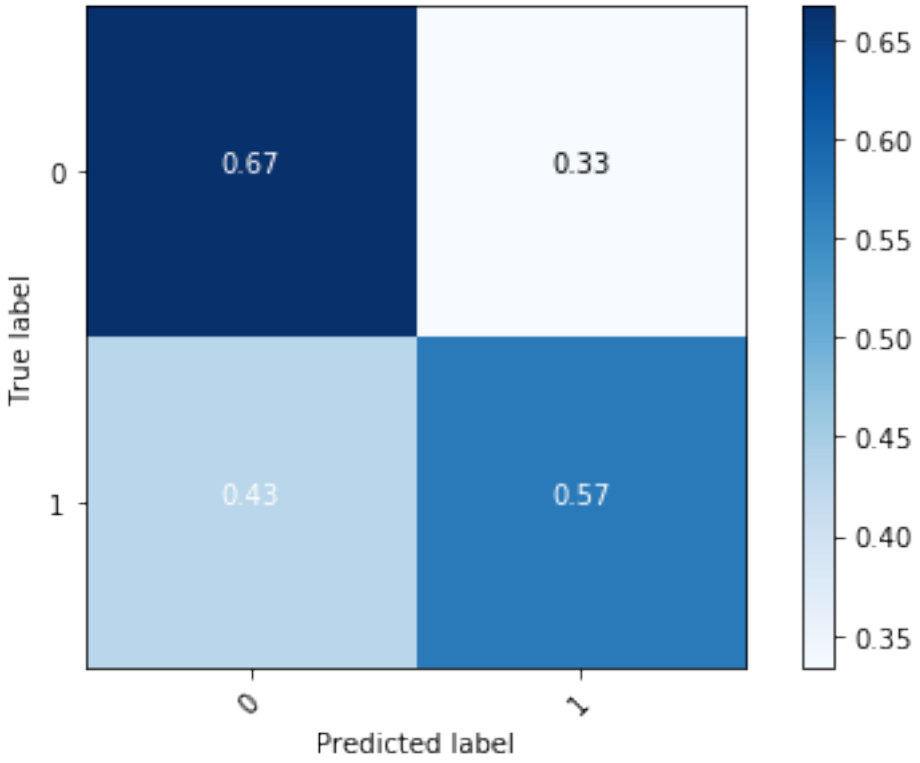
6.1 Evaluating the Algorithm

[18]:
```
forest = RandomForestClassifier(
    criterion='entropy',
    n_estimators=40,
    random_state=0
)

forest.fit(X_train, y_train)

y_pred = forest.predict(X_test)
```

```
print(classification_report(y_test,y_pred))
print(accuracy_score(y_test, y_pred))
```

```
              precision    recall  f1-score   support

         0.0       0.57      0.67      0.62         6
         1.0       0.67      0.57      0.62         7

    accuracy                           0.62        13
   macro avg       0.62      0.62      0.62        13
weighted avg       0.62      0.62      0.62        13

0.6153846153846154
```

[19]:
```
import itertools


cnf_matrix = confusion_matrix(y_test, y_pred)

def plot_confusion_matrix(cm, classes):
    cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]

    cmap=plt.cm.Blues

    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, format(cm[i, j], ".2f"),
                 horizontalalignment="center",
                 color="white" if cm[i, j] > thresh else "black")

    plt.tight_layout()
    plt.ylabel('True label')
    plt.xlabel('Predicted label')

n_classes=["0","1"]
plot_confusion_matrix(cnf_matrix, classes=n_classes)
```



7 Run Prediction

[20]:
```
result = forest.predict(dfDataSetToPredict[[
    "pedido.data.attributes.age",
    "pedido.data.attributes.diagnostic_main",
    "respuesta.articlesRevisedYear",
    "respuesta.pubmed_keys",
    "articulo"
]])

result
```

[20]:
```
array([1., 1., 1., …, 1., 0., 0.])
```