

# S4 - HOPE random forest-V2

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 \
0                75.0                FISTULA PERITONEAL
1                75.0                FISTULA PERITONEAL
2                75.0                FISTULA PERITONEAL
3                75.0                FISTULA PERITONEAL
4                75.0                FISTULA PERITONEAL
5                75.0                FISTULA PERITONEAL
6                75.0                FISTULA PERITONEAL
7                75.0                FISTULA PERITONEAL
8                75.0                FISTULA PERITONEAL
9                75.0                FISTULA PERITONEAL

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

Expand pubmed\_keys attribute

```
[4]: dfOrg['respuesta.pubmed_keys'] = dfOrg['respuesta.pubmed_keys'].apply(lambda x :
    ↪ str(x).split(','))

dfOrg = dfOrg.explode('respuesta.pubmed_keys').reset_index(drop=True)

dfOrg.head(10)
```

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

	pedido.data.attributes.gender	articulo	respuesta.articlesRevisedYear \
0	male	27395425	2018

1	male	27395425	2018
2	male	27395425	2018
3	male	27395425	2018
4	male	27395425	2018
5	male	27395425	2018
6	male	27395425	2018
7	male	27395425	2018
8	male	27395425	2018
9	male	27395425	2018

	respuesta.articlesRevisedMonth	respuesta.pubmed_keys	utilidad
0	1	Abdomen	1.0
1	1	Adenocarcinoma	1.0
2	1	Antiemetics	1.0
3	1	Blood Culture	1.0
4	1	Catharsis	1.0
5	1	Diuresis	1.0
6	1	Fistula	1.0
7	1	Gastrectomy	1.0
8	1	Incisional Hernia	1.0
9	1	Intestines	1.0

## 2 Transform (factorize) from Categories to continuous atributes

Transform 'pedido.data.attributes.diagnostic\_main' attribute

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

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

Transform 'gender' attribute

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

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

Transform 'respuesta.pubmed\_keys' attribute

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

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

total: 353

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

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

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

```
[9]: 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  27395425                                2018
2                                0  27395425                                2018
3                                0  27395425                                2018
4                                0  27395425                                2018
5                                0  27395425                                2018
6                                0  27395425                                2018
7                                0  27395425                                2018
8                                0  27395425                                2018
9                                0  27395425                                2018

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

```
[10]: 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 => 14758

```

Remove row with age eq NaN

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

### 3 Standardize the Data

Chooosed “age”, “diagnostic\_main”, “month” and “pubmed\_keys” attributes (based on PCA\_V3 study)

```

[12]: from sklearn.preprocessing import StandardScaler

features = ["pedido.data.attributes.age",
            "pedido.data.attributes.diagnostic_main",
            "respuesta.articlesRevisedMonth",
            "respuesta.pubmed_keys",
            "utilidad"
]

# 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
```

```
[12]: pedido.data.attributes.age  pedido.data.attributes.diagnostic_main  \
0          1.285887          -1.503163
1          1.285887          -1.503163
2          1.285887          -1.503163
3          1.285887          -1.503163
4          1.285887          -1.503163
...          ...          ...
15583      -0.607930          -0.586347
15584      -0.607930          -0.586347
15585      -0.607930          -0.586347
15586      -0.607930          -0.586347
15587      -0.607930          -0.586347

      respuesta.articlesRevisedMonth  respuesta.pubmed_keys  utilidad
0          -1.463658          -1.089722          1.0
1          -1.463658          -1.080463          1.0
2          -1.463658          -1.071203          1.0
3          -1.463658          -1.061944          1.0
4          -1.463658          -1.052684          1.0
...          ...          ...          ...
15583      -1.178433          -0.330441          NaN
15584      -1.178433          -0.978608          NaN
15585      -1.178433          0.891817          NaN
15586      -1.178433          -0.876753          NaN
15587      -1.178433          0.901077          NaN

[15578 rows x 5 columns]
```

## 4 Separe data by utilidad is defined

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

print(dfDataSetComplete.shape[0])

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

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

```
830
14748
```

## 5 Random Forest

We check the number of results

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

```
[14]: utilidad
      0.0    346
      1.0    484
      dtype: int64
```

Separate “utilidad” attribute from dataToTrain

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

```
[15]: (830, 4)
```

```
[16]: 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>

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

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

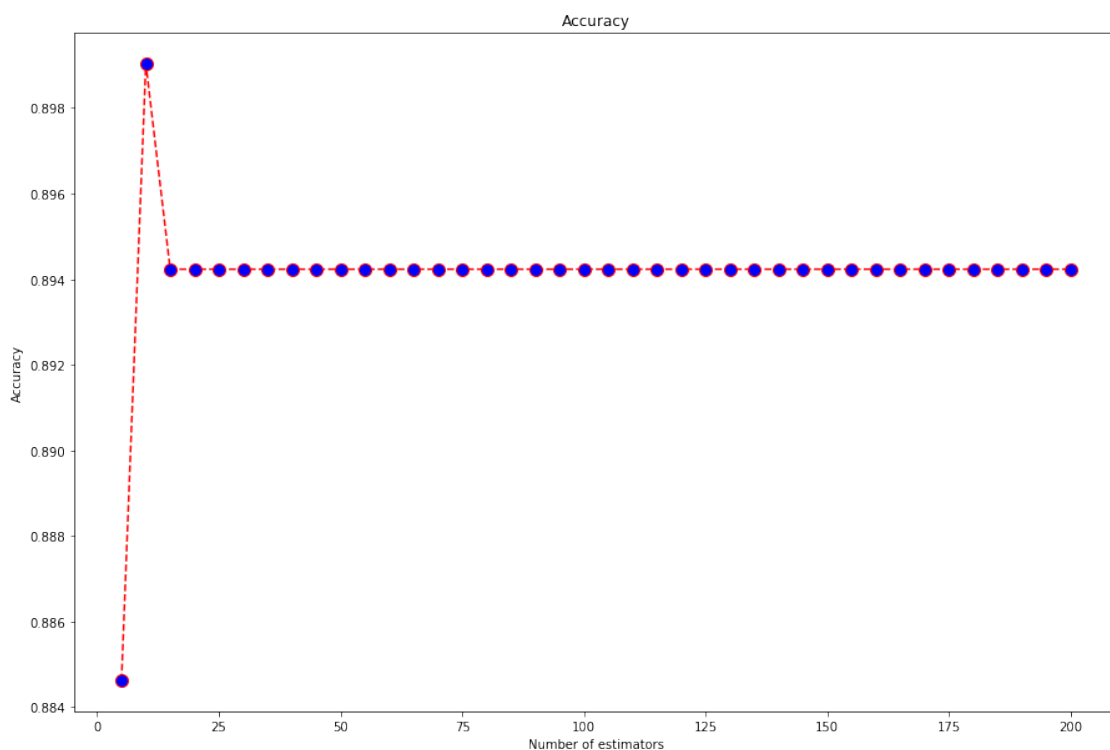
      for k in k_range:
          forest_test = RandomForestClassifier(
              criterion='entropy',
              n_estimators=k,
              random_state=0
          )
          forest_test.fit(X_train, y_train)
          y_pred_test = forest_test.predict(X_test)
```

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

```
[18]: 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')
```

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



## 6.1 Evaluating the Algorithm

```
[19]: forest = RandomForestClassifier(
        criterion='entropy',
        n_estimators=10,
        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	0.93	0.84	0.88	95
1.0	0.88	0.95	0.91	113
accuracy			0.90	208
macro avg	0.90	0.89	0.90	208
weighted avg	0.90	0.90	0.90	208

0.8990384615384616

```

[20]: 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

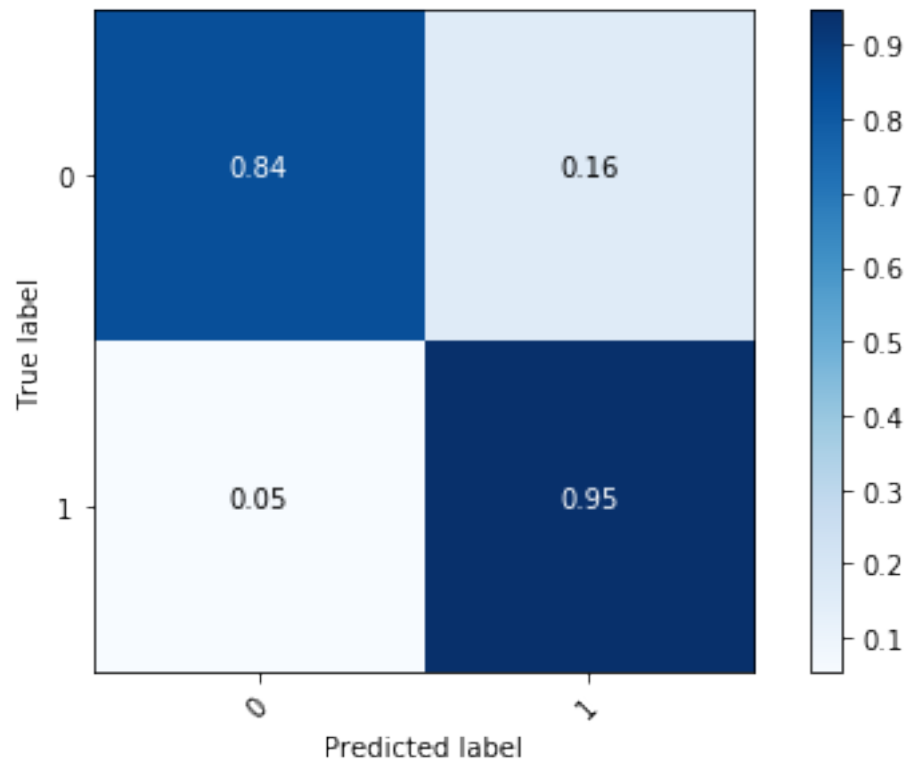
    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    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

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

result
```

```
[21]: array([1., 1., 1., ..., 0., 0., 0.])
```