## **Random Forest Classification**

#### **Import Libraries**

```
In [ ]: # import libraries
import numpy as np
import pandas as pd
```

#### **Load Dataset**

7.039e-02]])

```
In [ ]: #Load dataset
        from sklearn.datasets import load_breast_cancer
        data = load breast cancer()
In [ ]:
       data.data
Out[3]: array([[1.799e+01, 1.038e+01, 1.228e+02, ..., 2.654e-01, 4.601e-01,
                1.189e-01],
               [2.057e+01, 1.777e+01, 1.329e+02, ..., 1.860e-01, 2.750e-01,
                8.902e-02],
               [1.969e+01, 2.125e+01, 1.300e+02, ..., 2.430e-01, 3.613e-01,
                8.758e-02],
               [1.660e+01, 2.808e+01, 1.083e+02, ..., 1.418e-01, 2.218e-01,
                7.820e-02],
               [2.060e+01, 2.933e+01, 1.401e+02, ..., 2.650e-01, 4.087e-01,
                1.240e-01],
               [7.760e+00, 2.454e+01, 4.792e+01, ..., 0.000e+00, 2.871e-01,
```

```
data.target
In [ ]:
0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0,
             1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 0, 0,
             1, 1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1, 1, 0, 1,
             1, 1, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0,
             0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1,
             1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1,
             1, 0, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 0, 0,
             0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0,
             1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 1, 1, 0, 0, 1, 0, 1, 1,
             0, 0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 1,
             1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 1, 1,
             1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0,
             0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0,
             0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0,
             1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1, 1, 0, 0, 1, 1,
             1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0,
             1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1,
             1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0,
             1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
             1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1,
             1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
             1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
             1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1
      data.target names
Out[6]: array(['malignant', 'benign'], dtype='<U9')</pre>
```

localhost:8888/notebooks/mL imp/algoritham/Save Model.ipynb

In [ ]: # create dtaframe
df = pd.DataFrame(np.c\_[data.data, data.target], columns=[list(data.feature\_names)+['target']])
df.head()

#### Out[7]:

								mean		mean	
	mean 	mean	mean	mean	mean	mean	mean	concave	mean	fractal	r
	radius	texture	perimeter	area	smoothness	compactness	concavity	points	symmetry	dimension	
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07871	
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05667	
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05999	
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09744	
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05883	

4

In [ ]: df.tail()

#### Out[8]:

								mean		mean
	mean 	mean	mean	mean	mean	mean	mean	concave	mean	fractal
	radius	texture	perimeter	area	smoothness	compactness	concavity	points	symmetry	dimension
564	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0.1726	0.05623
565	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0.1752	0.05533
566	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0.1590	0.05648
567	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0.2397	0.07016
568	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0.1587	0.05884

4

```
In [ ]: df.shape
Out[9]: (569, 31)
```

#### **Split Data**

```
In []: X = df.iloc[:, 0:-1]
y = df.iloc[:, -1]

In []: from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=2020)

print('Shape of X_train = ', X_train.shape)
print('Shape of y_train = ', y_train.shape)
print('Shape of X_test = ', X_test.shape)
print('Shape of y_test = ', y_test.shape)

Shape of X_train = (455, 30)
Shape of y_train = (455,)
Shape of y_test = (114, 30)
Shape of y_test = (114,)
```

### **Train Random Forest Classification Model**

```
In [ ]: from sklearn.ensemble import RandomForestClassifier
```

### **Predict Cancer**

Out[14]: 0.956140350877193

```
In [ ]: patient1 = [17.99,
         10.38,
         122.8,
         1001.0,
         0.1184,
         0.2776,
         0.3001,
         0.1471,
         0.2419,
         0.07871,
         1.095,
         0.9053,
         8.589,
         153.4,
         0.006399,
         0.04904,
         0.05373,
         0.01587,
         0.03003,
         0.006193,
         25.38,
         17.33,
         184.6,
         2019.0,
         0.1622,
         0.6656,
         0.7119,
         0.2654,
         0.4601,
         0.1189]
```

```
In [ ]: patient1 = np.array([patient1])
         patient1
Out[16]: array([[1.799e+01, 1.038e+01, 1.228e+02, 1.001e+03, 1.184e-01, 2.776e-01,
                 3.001e-01, 1.471e-01, 2.419e-01, 7.871e-02, 1.095e+00, 9.053e-01,
                 8.589e+00, 1.534e+02, 6.399e-03, 4.904e-02, 5.373e-02, 1.587e-02,
                 3.003e-02, 6.193e-03, 2.538e+01, 1.733e+01, 1.846e+02, 2.019e+03,
                 1.622e-01, 6.656e-01, 7.119e-01, 2.654e-01, 4.601e-01, 1.189e-01]])
In [ ]: classifier.predict(patient1)
Out[17]: array([0.])
In [ ]: data.target names
Out[18]: array(['malignant', 'benign'], dtype='<U9')</pre>
In [ ]: pred = classifier.predict(patient1)
In [ ]: if pred[0] == 0:
           print('Patient has Cancer (malignant tumor)')
         else:
           print('Patient has no Cancer (malignant benign)')
         Patient has Cancer (malignant tumor)
```

### Save Model

## **Save Model using Pickle**

```
In [ ]: import pickle
```

```
In [ ]: pickle.dump(classifier, open('model_save', 'wb'))
In [ ]: model = pickle.load(open('model_save', 'rb'))
In [ ]: model.predict(patient1)[0]
Out[37]: 0.0
```

# **Save Model using Joblib**

```
In []: import joblib
In []: joblib.dump(classifier, 'model_save2')
Out[40]: ['model_save2']
In []: model2 = joblib.load('model_save2')
In []: model2.predict(patient1)
Out[42]: array([0.])
```

Ab milenge next tutorial me, Tab tak ke liye SIKHATE SIKHATE kuch IMPLEMENT karte raho, Thank You....-:)