DNA Classification Using Machine Learning

About :

In this project, we will explore the world of bioinformatics by using Markov models, K-nearest neighbor (KNN) algorithms, support vector machines, and other common classifiers to classify short E. Coli DNA sequences. This project will use a dataset from the UCI Machine Learning Repository that has 106 DNA sequences, with 57 sequential nucleotides (“base-pairs”) each.

It includes :

- Importing data from the UCI repository
- Converting text inputs to numerical data
- Building and training classification algorithms
- Comparing and contrasting classification algorithms

In [1]:

```
# Hide warnings
import warnings
warnings.simplefilter('ignore')
```

Step 1: Importing the Dataset

The following code cells will import necessary libraries and import the dataset from the UCI repository as a Pandas DataFram

In [2]:

```
#import and change module name
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
url = 'https://archive.ics.uci.edu/ml/machine-learning-databases/molecular-biology/promo
names = ['Class', 'id', 'Sequence']
data = pd.read_csv(url, names = names)
```

In [3]:

```
data.columns
```

Out[3]:

```
Index(['Class', 'id', 'Sequence'], dtype='object')
```

In [4]:

```
data.head()
```

Out[4]:

	Class	id	Sequence
0	+	S10	\t\ttactagcaatacgcttgcgttcggtggttaagtatgtataat...
1	+	AMPC	\t\ttgctatcctgacagttgtcacgctgattggtgtcgttacaat...
2	+	AROH	\t\tgtactagagaactagtgcattagcttatttttttgttatcat...
3	+	DEOP2	\taattgtgatgtgtatcgaagtgtgttgcggagtagatgttagaa...
4	+	LEU1_TRNA	\ttcgataattaactattgacgaaaagctgaaaaccactagaatgc...

In [5]:

```
data.shape
```

```
(106, 3)
```

Out[5]:

In [6]:
```
data.dtypes
```

Out[6]:
```
Class       object
id          object
Sequence    object
dtype: object
```

Step 2: Preprocessing the Dataset

The data is not in a usable form; as a result, we will need to process it before using it to train our algorithms.

In [7]:
```
# Build our dataset using custom pandas dataframe
clases = data.loc[:,'Class']
clases.head()
```

Out[7]:
```
0    +
1    +
2    +
3    +
4    +
Name: Class, dtype: object
```

In [8]:
```
# generate list of DNA sequence
sequence = list(data.loc[:, 'Sequence'])
sequence
```

Out[8]:
```
['\t\ttactagcaatacgcttgcgttcggtggttaagtatgtataatgcgcgggcttgtcgt',
 '\t\ttgctatcctgacagttgtcacgctgattggtgtcgttacaatctaacgcatcgccaa',
 '\t\tgtactagagaactagtgcattagcttatttttttgttatcatgctaaccacccggcg',
 '\taattgtgatgtgtatcgaagtgtgttgcggagtagatgttagaatactaacaaactc',
 '\ttcgataattaactattgacgaaaagctgaaaaccactagaatgcgcctccgtggtag',
 '\taggggcaaggaggatggaaagaggttgccgtataaagaaactagagtccgtttaggt',
 '\t\tcaggggtggaggatttaagccatctcctgatgacgcatagtcagcccatcatgaat',
 '\t\ttttctacaaaacacttgatactgtatgagcatacagtataattgcttcaacagaaca',
 '\t\tcgacttaatatactgcgacaggacgtccgttctgtgtaaatcgcaatgaaatggttt',
 '\ttttaaatttcctcttgtcaggccggaataactccctataatgcgccaccactgaca',
 '\tgcaaaaataaatgcttgactctgtagcgggaaggcgtattatgcacaccccgcgccg',
 '\tcctgaaattcagggttgactctgaaagaggaaagcgtaatatacgccacctcgcgac',
 '\tgatcaaaaaaatacttgtgcaaaaaattgggatccctataatgcgcctccgttgaga',
 '\tctgcaatttttctattgcggcctgcggagaactccctataatgcgcctccatcgaca',
 '\ttttatatttttcgcttgtcaggccggaataactccctataatgcgccaccactgaca',
 '\taagcaaagaaatgcttgactctgtagcgggaaggcgtattatgcacaccgccgcgcc',
 '\tatgcatttttccgcttgtcttcctgagccgactccctataatgcgcctccatcgaca',
 '\t\taaacaatttcagaatagacaaaaactctgagtgtaataatgtagcctcgtgtcttgc',
 '\t\tctcaacgtaacactttacagcggcgcgtcatttgatatgatgcgccccgcttcccg',
 '\t\tgcaaataatcaatgtggacttttctgccgtgattatagacacttttgttacgcgttt',
 '\t\tgacaccatcgaatggcgcaaaacctttcgcggtatggcatgatagcgcccggaagag',
 '\t\taaaaacgtcatcgcttgcattagaaaggtttctggccgaccttataaccattaatta',
 '\t\ttctgaaatgagctgttgacaattaatcatcgaactagttaactagtacgcaagttca',
 '\taccggaagaaaaccgtgacattttaacacgtttgttacaaggtaaaggcgacgccgc',
 '\t\taaattaaaattttattgacttaggtcactaaatactttaaccaatataggcatagcg',
 '\t\tttgtcataatcgacttgtaaaccaaattgaaaagatttaggtttacaagtctacacc',
 '\t\tcatcctcgcaccagtcgacgacggtttacgctttacgtatagtggcgacaattttt',
 '\ttccagtataatttgttggcataattaagtacgacgagtaaaattacatacctgcccg',
 '\tacagttatccactattcctgtggataaccatgtgtattagagttagaaaacacgagg',
 '\t\ttgtgcagtttatggttccaaaatcgccttttgctgtatatactcacagcataactgt',
 '\tctgttgttcagtttttgagttgtgtataacccctcattctgatcccagcttatacgg',
 '\tattacaaaaagtgctttctgaactgaacaaaaaagagtaaagttagtcgcgtagggt',
 '\tatgcgcaacgcggggtgacaagggcgcgcaaaccctctatactgcgcgccgaagctg',
 '\t\tttaaaaaactaacagttgtcagcctgtcccgcttataagatcatacgccgttatacgt',
 '\t\tatgcaatttttttagttgcatgaactcgcatgtctccatagaatgcgcgctacttgat',
 '\tccttgaaaaagaggttgacgctgcaaggctctatacgcataatgcgccccgcaacgc',
 '\t\ttcgttgtatatttcttgacacctttcggcatcgccctaaaattcggcgtcctcata',
 '\t\tccgtttatttttctacccatatccttgaagcggtgttataatgccgcgccctcgat',
 '\t\ttttcgcatatttttcttgcaaagttgggttgagctggctagattagccagccaatctt',
 '\t\ttgtaaactaatgcctttacgtgggcggtgattttgtctacaatcttacccccacgta',
 '\tgatcgcacgatctgtatacttatttgagtaaattaacccacgatcccagccattctt',
 '\t\taacgcatacggtattttaccttcccagtcaagaaaacttatcttattcccactttc',
 '\tttagcggatcctacctgacgctttttatcgcaactctctactgtttctccatacccg',
 '\t\ttgccttctccaaaacgtgtttttgttgttaattcggtgtagacttgtaaacctaaat',
 '\tcagaaacgttttattcgaacatcgatctcgtcttgtgttagaattctaacatacggt',
 '\tcactaatttattccatgtcacacttttcgcatctttgttatgctatggttatttcat',
 '\t\ttatataaaaaagttcttgctttctaacgtgaaagtggtttaggttaaaagacatcagt',
 '\t\ttcaaggtagaatgctttgccttgtcggcctgattaatggcacgatagtcgcatcggat',
 '\tggccaaaaaatatcttgtactatttacaaaacctatggtaactctttaggcattcct',
 '\tttaggcaccccaggctttacactttatgcttccggctcgtatgttgtgtggaattgtg',
 '\t\ttccatcaaaaaaatattctcaacataaaaaactttgtgtaatacttgtaacgctacat',
 '\t\tttggggacgtcgttactgatccgcacgtttatgatatgctatcgtactctttagcgag',
 '\tttcagaaatattatggtgatgaactgtttttttatccagtataatttgttggcataat',
 '\t\ttatatgaacgttgagactgccgctgagttatcagctgtgaacgacattctggcgtcta',
 '\t\ttcgaacgagtcaatcagaccgctttgactctggtattactgtgaacattattcgtctc',
 '\t\ttcaatggcctctaaacgggtcttgagggggtttttttgctgaaaggaggaactatatgcg',
 '\t\ttttgacctactacgccagcattttggcggtgtaagctaaccattccggttgactcaat',
 '\t\ttcgtctatcggtgaacctccggtatcaacgctggaaggtgacgctaacgcagatgcag',
 '\t\ttgccaatcaatcaagaacttgaagggtggtatcagccaacagcctgacatccttcgtt',
 '\t\tttggatggacgttcaacattgaggaaggcataacgctactacctgatgtttactccaa',
 '\t\ttgaggtggctatgtgtatgaccgaacgagtcaatcagaccgctttgactctggtatta',
 '\t\ttcgtagcgcatcagtgctttcttactgtgagtacgcaccagcgccagaggacgacgac',
 '\t\ttcgaccgaagcgagcctcgtcctcaatggcctctaaacgggtcttgagggggtttttttg',
 '\t\ttctacggtgggtacaatatgctggatggagatgcgttcacttctggtctactgactcg',
 '\t\ttatagtctcagagtcttgacctactacgccagcattttggcggtgtaagctaaccatt',
 '\t\ttaactcaaggctgatacggcgagacttgcgagccttgtccttgcggtacacagcagcg',
 '\t\ttttactgtgaacattattcgtctccgcgactacgatgagatgcctgagtgcttccgtt',
 '\t\tttattctcaacaagattaaccgacagattcaatctcgtggatggacgttcaacattga',
 '\t\ttaacgagtcaatcagaccgctttgactctggtattactgtgaacattattcgtctccg',
 '\t\ttaagtgcttagcttcaaggtcacggatacgaccgaagcgagcctcgtcctcaatggcc',
 '\t\ttgaagaccacgcctcgccaccgagtagacccttagagagcatgtcagcctcgacaact',
 '\t\ttttagagagcatgtcagcctcgacaacttgcataaatgctttcttgtagacgtgccct',
 '\t\tttattcgtctccgcgactacgatgagatgcctgagtgcttccgttactggattgtcac',
 '\t\tttgctgaaaggaggaactatatgcgctcatacgatatgaacgttgagactgccgctga',
 '\t\ttcatgaactcaaggctgatacggcgagacttgcgagccttgtccttgcggtacacagc',
 '\t\ttttcgtctccgcgactacgatgagatgcctgagtgcttccgttactggattgtcacca',
 '\t\ttcatgtcagcctcgacaacttgcataaatgctttcttgtagacgtgccctacgcgctt',
 '\t\ttaggaggaactacgcaaggttggaacatcggagagatgccagccagcgcacctgcacg',
 '\t\tttctcaacaagattaaccgacagattcaatctcgtggatggacgttcaacattgagga',
 '\t\tttgaagtgcttagcttcaaggtcacggatacgaccgaagcgagcctcgtcctcaatgg',
 '\t\ttctatatgcgctcatacgatatgaacgttgagactgccgctgagttatcagctgtgaa',
 '\t\ttgcggcagcacgtttccacgcggtgagagcctcaggattcatgtcgatgtcttccggt',
 '\t\ttatccctaatgtctacttccggtcaatccatctacgttaaccgaggtggctatgtgta',
 '\t\tttggcgtctatcggtgaacctccggtatcaacgctggaaggtgacgctaacgcagatg',
 '\t\tttctcgtggatggacgttcaacattgaggaaggcataacgctactacctgatgtttac',
 '\t\tttattggcttgctcaagcatgaactcaaggctgatacggcgagacttgcgagccttgt',
 '\t\tttagagggtgtactccaagaagaggaagatgaggctagacgtctctgcatggagtatg',
 '\t\ttcagcggcagcacgtttccacgcggtgagagcctcaggattcatgtcgatgtcttccg',
 '\t\ttttacgttggcgaccgctaggactttcttgttgattttccatgcggtgttttgcgcaa',
 '\t\ttacgctaacgcagatgcagcgaacgctcggcgtattctcaacaagattaaccgacaga',
 '\t\ttggtgttttgcgcaatgttaatcgctttgtacacctcaggcatgtaaacgtcttcgta',
 '\t\ttaaccattccggttgactcaatgagcatctcgatgcagcgtactcctacatgaataga',
 '\t\ttagacgtctctgcatggagtatgagatggactacggtgggtacaatatgctggatgga',
 '\t\tttgttgattttccatgcggtgttttgcgcaatgttaatcgctttgtacacctcaggca',
 '\t\tttgcacgggttgcgatagcctcagcgtattcaggtgcgagttcgatagtctcagagtc',
 '\t\ttaggcatgtaaacgtcttcgtagcgcatcagtgctttcttactgtgagtacgcaccag',
 '\t\ttccgagtagacccttagagagcatgtcagcctcgacaacttgcataaatgctttcttg',
 '\t\ttcgctaggactttcttgttgattttccatgcggtgttttgcgcaatgttaatcgcttt',
 '\t\tttatgaccgaacgagtcaatcagaccgctttgactctggtattactgtgaacattatt',
 '\t\ttagagggtgtactccaagaagaggaagatgaggctagacgtctctgcatggagtatga',
 '\t\ttgagagcatgtcagcctcgacaacttgcataaatgctttcttgtagacgtgccctacg',
 '\t\ttcctcaatggcctctaaacgggtcttgagggggtttttttgctgaaaggaggaactatat',
  '\t\tgtattctcaacaagattaaccgacagattcaatctcgtggatggacgttcaacattg',
  '\t\tcgcgactacgatgagatgcctgagtgcttccgttactggattgtcaccaaggcttcc',
  '\t\tctcgtcctcaatggcctctaaacgggtcttgaggggtttttttgctgaaaggaggaac',
  '\t\tttaacattaataaataaggaggctctaatggcactcattagccaatcaatcaagaact']
```

In [9]:

```python
#Remove tab from each sequence
dic = {}
for i, seq in enumerate(sequence):
    nucleotides = list(seq)
    nucleotides = [char for char in nucleotides if char != '\t']
    #append class assignment
    nucleotides.append(clases[i])

    dic[i] = nucleotides
dic[0]
```

Out[9]:

```
['t',
 'a',
 'c',
 't',
 'a',
 'g',
 'c',
 'a',
 'a',
 't',
 'a',
 'c',
 'g',
 'c',
 't',
 't',
 'g',
 'c',
 'g',
 't',
 't',
 'c',
 'g',
 'g',
 't',
 'g',
 'g',
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 't',
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 'g',
 't',
 'a',
 't',
 'a',
 'a',
 't',
 'g',
 'c',
 'g',
 'c',
 'g',
 'g',
 'g',
 'c',
 't',
 't',
 'g',
 't',
 'c',
 'g',
 't',
 '+']
```

In [10]:

```
# Convert Dict object into dataframe
df = pd.DataFrame(dic)
df.head()
```

Out[10]:

	0	1	2	3	4	5	6	7	8	9	...	96	97	98	99	100	101	102	103	104	105
0	t	t	g	a	t	a	c	t	c	t	...	c	c	t	a	g	c	g	c	c	t
1	a	g	t	a	c	g	a	t	g	t	...	c	g	a	g	a	c	t	g	t	a
2	c	c	a	t	g	g	g	t	a	t	...	g	c	t	a	g	t	a	c	c	a
3	t	t	c	t	a	g	g	c	c	t	...	a	t	g	g	a	c	t	g	g	c
4	a	a	t	g	t	g	g	t	t	a	...	g	a	a	g	g	a	t	a	t	a

5 rows × 106 columns

In [11]:

```
# transpose dataframe into correct format
df = df.transpose()
df.head()
```

Out[11]:

	0	1	2	3	4	5	6	7	8	9	...	48	49	50	51	52	53	54	55	56	57
0	t	a	c	t	a	g	c	a	a	t	...	g	c	t	t	g	t	c	g	t	+
1	t	g	c	t	a	t	c	c	t	g	...	c	a	t	c	g	c	c	a	a	+
2	g	t	a	c	t	a	g	a	g	a	...	c	a	c	c	c	g	g	c	g	+
3	a	a	t	t	g	t	g	a	t	g	...	a	a	c	a	a	a	c	t	c	+
4	t	c	g	a	t	a	a	t	t	a	...	c	c	g	t	g	g	t	a	g	+

5 rows × 58 columns

In [12]:

```
df.columns
```

Out[12]:

```
RangeIndex(start=0, stop=58, step=1)
```

In [13]:

```
# Rename
df.rename(columns = {57:'Class'}, inplace = True)
```

In [14]:

```
df.columns
```

Out[14]:

```
Index([      0,        1,        2,        3,        4,        5,        6,        7,
             8,        9,       10,       11,       12,       13,       14,       15,
            16,       17,       18,       19,       20,       21,       22,       23,
            24,       25,       26,       27,       28,       29,       30,       31,
            32,       33,       34,       35,       36,       37,       38,       39,
            40,       41,       42,       43,       44,       45,       46,       47,
            48,       49,       50,       51,       52,       53,       54,       55,
            56, 'Class'],
      dtype='object')
```

In [15]:

```
df.head()
```

Out[15]:

	0	1	2	3	4	5	6	7	8	9	...	48	49	50	51	52	53	54	55	56	Class
0	t	a	c	t	a	g	c	a	a	t	...	g	c	t	t	g	t	c	g	t	+
1	t	g	c	t	a	t	c	c	t	g	...	c	a	t	c	g	c	c	a	a	+
2	g	t	a	c	t	a	g	a	g	a	...	c	a	c	c	c	g	g	c	g	+
3	a	a	t	t	g	t	g	a	t	g	...	a	a	c	a	a	a	c	t	c	+
4	t	c	g	a	t	a	a	t	t	a	...	c	c	g	t	g	g	t	a	g	+

5 rows × 58 columns

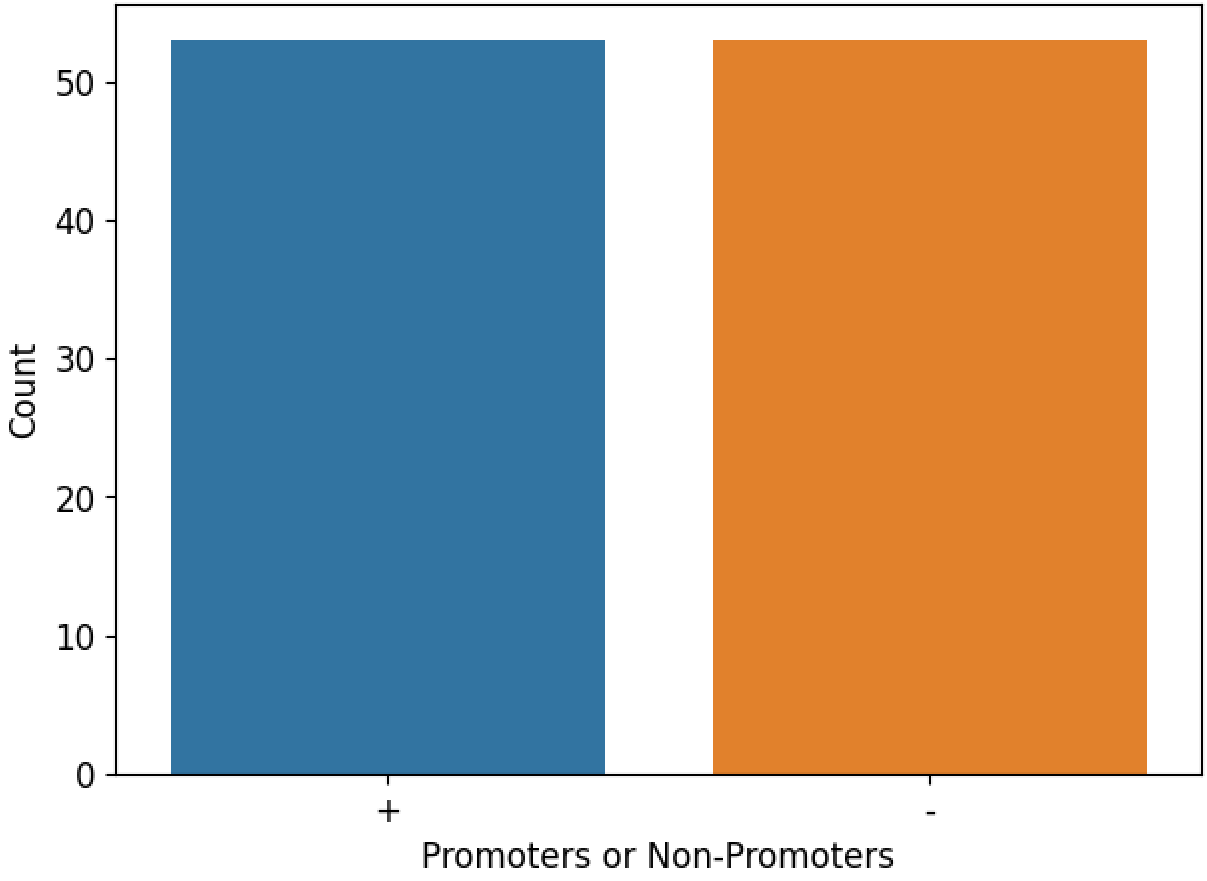
In [29]:

```python
import matplotlib.pyplot as plt
import seaborn as sns

# Assuming 'df' is your DataFrame with a column named 'Class'
plt.figure(figsize=(7, 5))
ax = sns.countplot(x="Class", data=df)

plt.xticks(size=12)
plt.xlabel("Promoters or Non-Promoters", size=12)
plt.yticks(size=12)
plt.ylabel("Count", size=12)

plt.savefig("target_histogram.png")
plt.show()
```



In [16]:

```python
#Encoding
numerical_df = pd.get_dummies(df)
numerical_df.head()
```

Out[16]:

	0_a	0_c	0_g	0_t	1_a	1_c	1_g	1_t	2_a	2_c	...	55_a	55_c	55_g	55_t	56_a	56
0	False	False	False	True	True	False	False	False	False	True	...	False	False	True	False	False	Fal

1	False	False	False	True	False	False	True	False	False	True	...	True	False	False	False	True	Fal
2	False	False	True	False	False	False	False	True	True	False	...	False	True	False	False	False	Fal
3	True	False	False	False	True	False	False	False	False	False	...	False	False	False	True	False	Tr
4	False	False	False	True	False	True	False	False	False	False	...	True	False	False	False	False	Fal

5 rows × 230 columns

In [17]:

```
# Drop class_- or Class_+ either of one
numerical_df.drop('Class_-', axis = 1, inplace = True)
numerical_df.head()
```

Out[17]:

	0_a	0_c	0_g	0_t	1_a	1_c	1_g	1_t	2_a	2_c	...	54_t	55_a	55_c	55_g	55_t	56
0	False	False	False	True	True	False	False	False	False	True	...	False	False	False	True	False	Fal
1	False	False	False	True	False	False	True	False	False	True	...	False	True	False	False	False	Tr
2	False	False	True	False	False	False	False	True	True	False	...	False	False	True	False	False	Fal
3	True	False	False	False	True	False	False	False	False	False	...	False	False	False	False	True	Fal
4	False	False	False	True	False	True	False	False	False	False	...	True	True	False	False	False	Fal

5 rows × 229 columns

In [18]:

```
# rename Class_+ to Class
numerical_df.rename(columns = {'Class_+':'Class'}, inplace = True)
```

Step 3: Training and Testing the Classification Algorithms

Now that we have preprocessed the data and built our training and testing datasets, we can start to deploy different classification algorithms. It's relatively easy to test multiple models; as a result, we will compare and contrast the performance of ten different algorithms.

In [19]:

```
#Importing different classifier from sklearn
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn import svm
from sklearn.naive_bayes import GaussianNB
from sklearn.gaussian_process.kernels import RBF
from sklearn.gaussian_process import GaussianProcessClassifier
from sklearn.neural_network import MLPClassifier
from sklearn.ensemble import RandomForestClassifier, AdaBoostClassifier
from sklearn.metrics import classification_report, accuracy_score
```

In [20]:

```
from sklearn.model_selection import train_test_split
X = numerical_df.drop(['Class'], axis = 1).values
y = numerical_df['Class'].values

#define a seed for reproducibility
seed = 1

# Splitting data into training and testing data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.25, random_state
```

In [22]:

```
# Define scoring method
scoring = 'accuracy'
# Model building to train
names = ['K Nearest Neighbors', 'Gaussian Process', 'Decision Tree', 'Random Forest', 'N
```

```
Classifiers = [
    KNeighborsClassifier(n_neighbors = 3),
    GaussianProcessClassifier(1.0*RBF(1.0)),
    DecisionTreeClassifier(max_depth = 5),
    RandomForestClassifier(max_depth = 5, n_estimators = 10, max_features = 1 ),
    MLPClassifier(alpha = 1),
    AdaBoostClassifier(),
    GaussianNB(),
    svm.SVC(kernel = 'linear'),
    svm.SVC(kernel = 'rbf'),
    svm.SVC(kernel = 'sigmoid')

    ]
models = zip(names, Classifiers)
# import KFold
from sklearn.model_selection import KFold, cross_val_score

names = []
result = []
for name, model in models:
    kfold = KFold(n_splits = 10, random_state = 1, shuffle=True)
    cv_results = cross_val_score(model, X_train, y_train, cv = kfold, scoring = 'accurac
    result.append(cv_results)
    names.append(name)
    msg = "{0}: {1} ({2})".format(name, cv_results.mean(), cv_results.std())
    print(msg)
```

```
K Nearest Neighbors: 0.8107142857142857 (0.099808490089158)
Gaussian Process: 0.8553571428571429 (0.1606051216556957)
Decision Tree: 0.6928571428571428 (0.11539638872431081)
Random Forest: 0.6428571428571429 (0.20640261823999842)
Neural Net: 0.9125 (0.09762812094883318)
AdaBoost: 0.875 (0.1479019945774904)
Naive Bayes: 0.8375 (0.1125)
SVM Linear: 0.9125 (0.09762812094883318)
SVM RBF: 0.875 (0.11180339887498948)
SVM Sigmoid: 0.925 (0.1)
```

Step 4 : Model Evaluation

Now that we will evaluate our classification algorithms using accuracy score and classification report.

In [23]:

```
#Test the algorithm on the test data set
models = zip(names, Classifiers)
for name, model in models:
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    print(name)
    print(accuracy_score(y_test, y_pred))
    print(classification_report(y_test, y_pred))
```

```
K Nearest Neighbors
0.7777777777777778
              precision    recall  f1-score   support

       False       1.00      0.65      0.79        17
        True       0.62      1.00      0.77        10

    accuracy                           0.78        27
   macro avg       0.81      0.82      0.78        27
weighted avg       0.86      0.78      0.78        27

Gaussian Process
```

```
0.8888888888888888
              precision    recall  f1-score   support

       False       1.00      0.82      0.90        17
        True       0.77      1.00      0.87        10

    accuracy                           0.89        27
   macro avg       0.88      0.91      0.89        27
weighted avg       0.91      0.89      0.89        27

Decision Tree
0.7037037037037037
              precision    recall  f1-score   support

       False       0.91      0.59      0.71        17
        True       0.56      0.90      0.69        10

    accuracy                           0.70        27
   macro avg       0.74      0.74      0.70        27
weighted avg       0.78      0.70      0.71        27

Random Forest
0.5555555555555556
              precision    recall  f1-score   support

       False       0.73      0.47      0.57        17
        True       0.44      0.70      0.54        10

    accuracy                           0.56        27
   macro avg       0.58      0.59      0.55        27
weighted avg       0.62      0.56      0.56        27

Neural Net
0.9259259259259259
              precision    recall  f1-score   support

       False       1.00      0.88      0.94        17
        True       0.83      1.00      0.91        10

    accuracy                           0.93        27
   macro avg       0.92      0.94      0.92        27
weighted avg       0.94      0.93      0.93        27

AddaBoost
0.8518518518518519
              precision    recall  f1-score   support

       False       1.00      0.76      0.87        17
        True       0.71      1.00      0.83        10

    accuracy                           0.85        27
   macro avg       0.86      0.88      0.85        27
weighted avg       0.89      0.85      0.85        27

Naive Bayes
0.9259259259259259
              precision    recall  f1-score   support

       False       1.00      0.88      0.94        17
        True       0.83      1.00      0.91        10

    accuracy                           0.93        27
   macro avg       0.92      0.94      0.92        27
weighted avg       0.94      0.93      0.93        27

SVM Linear
```

```
0.9629629629629629
              precision    recall  f1-score   support

       False       1.00      0.94      0.97        17
        True       0.91      1.00      0.95        10

    accuracy                           0.96        27
   macro avg       0.95      0.97      0.96        27
weighted avg       0.97      0.96      0.96        27

SVM RBF
0.9259259259259259
              precision    recall  f1-score   support

       False       1.00      0.88      0.94        17
        True       0.83      1.00      0.91        10

    accuracy                           0.93        27
   macro avg       0.92      0.94      0.92        27
weighted avg       0.94      0.93      0.93        27

SVM Sigmoid
0.9259259259259259
              precision    recall  f1-score   support

       False       1.00      0.88      0.94        17
        True       0.83      1.00      0.91        10

    accuracy                           0.93        27
   macro avg       0.92      0.94      0.92        27
weighted avg       0.94      0.93      0.93        27
```

Conclusion :

From above report, Support Vector Machine with 'linear' kernel performed best with F1_score = 0.96 on testing data.

Thanks !