IDS_PROJECT

November 19, 2018

1 Problem Statement

Applying ML Classification algorithms on the data set and getting inferences from the data.

2 Data-Set

We have collected our dataset from the following link: https://www.kaggle.com/uciml/mushroom-classification. This data set includes descriptions of hypothetical samples corresponding to 23 species of gilled mushrooms in the Agaricus and Lepiota Family (pp. 500-525). Each species is identified as definitely edible or definitely poisonous. Number of Instances: 8124

3 Attributes

```
Number of Attributes: 22 (all nominally valued)
cap-shape: bell=b,conical=c,convex=x,flat=f, knobbed=k,sunken=s
cap-surface: fibrous=f,grooves=g,scaly=y,smooth=s
cap-color: brown=n,buff=b,cinnamon=c,gray=g,green=r,pink=p,purple=u,red=e,white=w,yellow=y
bruises: bruises=t,no=f
odor: almond=a,anise=l,creosote=c,fishy=y,foul=f,musty=m,none=n,pungent=p,spicy=s
gill-attachment: attached=a,descending=d,free=f,notched=n
gill-spacing: close=c,crowded=w,distant=d
gill-size: broad=b,narrow=n
gill-color: black=k,brown=n,buff=b,chocolate=h,gray=g, green=r,orange=o,pink=p,purple=u,red=e,
stalk-shape: enlarging=e,tapering=t
stalk-root: bulbous=b,club=c,cup=u,equal=e,rhizomorphs=z,rooted=r,missing=?
stalk-surface-above-ring: fibrous=f,scaly=y,silky=k,smooth=s
stalk-surface-below-ring: fibrous=f,scaly=y,silky=k,smooth=s
stalk-color-above-ring: brown=n,buff=b,cinnamon=c,gray=g,orange=o,pink=p,red=e,white=w,yellow=
stalk-color-below-ring: brown=n,buff=b,cinnamon=c,gray=g,orange=o,pink=p,red=e,white=w,yellow=
veil-type: partial=p,universal=u
veil-color: brown=n,orange=o,white=w,yellow=y
ring-number: none=n,one=o,two=t
ring-type: cobwebby=c,evanescent=e,flaring=f,large=l,none=n,pendant=p,sheathing=s,zone=z
spore-print-color: black=k,brown=n,buff=b,chocolate=h,green=r,orange=o,purple=u,white=w,yellow
population: abundant=a,clustered=c,numerous=n,scattered=s,several=v,solitary=y
habitat: grasses=g,leaves=l,meadows=m,paths=p,urban=u,waste=w,woods=d
```

4 Libraries

- NumPy(Numerical Python) gives an lot of useful things for linear algebra & operations on n-arrays.
- Pandas is a python package who is a perfect tool for data preprocessing.
- Matplotlib is a python library which is great in making data visulations.
- Seaborn is mostly focused on the visualization of statistical model.
- Scikit-learn exposes a concise & consistent interface to the common machine learning algorithms.

```
In [2]: #Allows charts to appear in notebook
        %matplotlib inline
        #Libraries
        import pandas as pan
        import numpy as nmp
        from sklearn import svm
        from sklearn.model_selection import train_test_split
        #Visual Libraries
        import matplotlib.pyplot as mpp
        import seaborn as sbn; sbn.set(font_scale=1.5)
        # Label Encoding
        from sklearn.preprocessing import LabelEncoder
        # Using for dividing the dataset in training dataset and testing dataset
        from sklearn.model_selection import train_test_split
        # Feature Scaling
        from sklearn.preprocessing import StandardScaler
```

5 Importing the file of Mushroom Dataset

```
In [3]: mushroom_dataframe = pan.read_csv("mushrooms.csv")
        mushroom_dataframe.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8124 entries, 0 to 8123
Data columns (total 23 columns):
class                       8124 non-null object
cap-shape                   8124 non-null object
cap-surface                 8124 non-null object
cap-color                   8124 non-null object
bruises                     8124 non-null object
odor                        8124 non-null object
gill-attachment             8124 non-null object
gill-spacing                8124 non-null object
gill-size                   8124 non-null object
gill-color                  8124 non-null object
stalk-shape                 8124 non-null object
stalk-root                  8124 non-null object
stalk-surface-above-ring    8124 non-null object
```

```
stalk-surface-below-ring    8124 non-null object
stalk-color-above-ring      8124 non-null object
stalk-color-below-ring      8124 non-null object
veil-type                   8124 non-null object
veil-color                  8124 non-null object
ring-number                 8124 non-null object
ring-type                   8124 non-null object
spore-print-color           8124 non-null object
population                  8124 non-null object
habitat                     8124 non-null object
dtypes: object(23)
memory usage: 1.4+ MB
```

6 Data Cleaning

Description of dataset says that data column 'stalk-root' has some missing values, represented by '?'. Data cleansing or data cleaning is the process of detecting and correcting (or removing) corrupt or inaccurate records from a dataset. So, we are going to exclude the data rows that contains these values in their 'stalk-root' column.

```
In [4]: mushroom_dataframe = mushroom_dataframe[mushroom_dataframe['stalk-root'] != '?']
```

7 Splitting non-class and class variables

```
In [6]: # Target dataset
        target = mushroom_dataframe['class']
        # Features(non-class variables) dataset
        features = mushroom_dataframe.drop(columns=['class'])
        # For checking purpose
        features.head()
```

```
Out[6]:   cap-shape cap-surface cap-color bruises odor gill-attachment gill-spacing  \
        0         x           s         n       t    p               f            c
        1         x           s         y       t    a               f            c
        2         b           s         w       t    l               f            c
        3         x           y         w       t    p               f            c
        4         x           s         g       f    n               f            w

          gill-size gill-color stalk-shape   ...   stalk-surface-below-ring  \
        0         n          k           e   ...                          s
        1         b          k           e   ...                          s
        2         b          n           e   ...                          s
        3         n          n           e   ...                          s
        4         b          k           t   ...                          s

          stalk-color-above-ring stalk-color-below-ring veil-type veil-color  \
        0                      w                      w         p          w
        1                      w                      w         p          w
        2                      w                      w         p          w
        3                      w                      w         p          w
        4                      w                      w         p          w

          ring-number ring-type spore-print-color population habitat
        0           o         p                 k          s       u
        1           o         p                 n          n       g
        2           o         p                 n          n       m
        3           o         p                 k          s       u
        4           o         e                 n          a       g

        [5 rows x 22 columns]
```

8 Data Transformation

Data transformation is the process of converting data or information from one format to another, usually from the format of a source system into the required format of a new destination system. This dataset is based on non-numeric data. Machine learning models are based on numeric data. So, we are going to convert this data into numeric .To accomplish this, we use built-in class of python called LabelEncoder.

```
In [7]: # Encoding non-class variables dataset
        Feature_Enc = LabelEncoder()
        for a in features.columns:
            features[a] = Feature_Enc.fit_transform(features[a])
        # Encoding class variable dataset
        Target_Enc = LabelEncoder()
        target = Target_Enc.fit_transform(target)
```

```
In [8]: target
```

```
Out[8]: array([1, 0, 0, ..., 0, 1, 1])
```

Here, we get 1 in place of poisonous value and 0 in place of edible value.

```
In [9]: features.head(10)
```

```
Out[9]:    cap-shape  cap-surface  cap-color  bruises  odor  gill-attachment  \
        0          5            2          4        1     6                1
        1          5            2          7        1     0                1
        2          0            2          6        1     3                1
        3          5            3          6        1     6                1
        4          5            2          3        0     5                1
        5          5            3          7        1     0                1
        6          0            2          6        1     0                1
        7          0            3          6        1     3                1
```

```
8          5           3          6        1     6                1
9          0           2          7        1     0                1

   gill-spacing  gill-size  gill-color  stalk-shape   ...     \
0             0          1           2            0   ...
1             0          0           2            0   ...
2             0          0           3            0   ...
3             0          1           3            0   ...
4             1          0           2            1   ...
5             0          0           3            0   ...
6             0          0           0            0   ...
7             0          0           3            0   ...
8             0          1           4            0   ...
9             0          0           0            0   ...

   stalk-surface-below-ring  stalk-color-above-ring  stalk-color-below-ring  \
0                         2                       5                       5
1                         2                       5                       5
2                         2                       5                       5
3                         2                       5                       5
4                         2                       5                       5
5                         2                       5                       5
6                         2                       5                       5
7                         2                       5                       5
8                         2                       5                       5
9                         2                       5                       5

   veil-type  veil-color  ring-number  ring-type  spore-print-color  \
0          0           0            1          3                  1
1          0           0            1          3                  2
2          0           0            1          3                  2
3          0           0            1          3                  1
4          0           0            1          0                  2
5          0           0            1          3                  1
6          0           0            1          3                  1
7          0           0            1          3                  2
8          0           0            1          3                  1
9          0           0            1          3                  1

   population  habitat
0           3        5
1           2        1
2           2        3
3           3        5
4           0        1
5           2        1
6           2        3
7           3        3
```

```
8            4        1
9            3        3

[10 rows x 22 columns]
```

Here also, you can see that categorical values are also changed into numerical values.

Now, we are going to change this features dataset into only 0,1 values using dummy variables. A Dummy variable is one that takes the value 0 or 1 to indicate the absence or presence of some categorical effect that may be expected to shift the outcome.

```
In [10]: features=pan.get_dummies(features,columns=features.columns,drop_first=True)
```

9 Breaking the dataset into Test Set and Training Set

Split dataset into random train and test subsets.

```
In [11]: featuresTrain, featuresTest, targetTrain, targetTest = train_test_split(features, targ
```

10 Data normalization(Feature Scaling)

Database normalization is the process of restructuring a relational database in accordance with a series of so-called normal forms in order to reduce data redundancy and improve data integrity. Feature scaling through standardization can be an important preprocessing step for many machine learning algorithms. Standardization involves rescaling the features such that they have the properties of a standard normal distribution with a mean of zero and a standard deviation of one.

```
In [14]: standardscaler = StandardScaler()
         featuresTrain = standardscaler.fit_transform(featuresTrain)
         featuresTest = standardscaler.transform(featuresTest)
```

11 Applying Principal Component Analysis

Principal Component Analysis (PCA) is a dimension-reduction tool that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set. We are using this to reduce 22 columns features dataset into only 2 variables features dataset.

```
In [15]: from sklearn.decomposition import PCA
         p_c_a = PCA(n_components=2)
         featuresTrain = p_c_a.fit_transform(featuresTrain)
         featuresTest = p_c_a.transform(featuresTest)
```

12 Algorithms

abc

```
In [33]: def training_visual(mdel):
             sbn.set_context(context='notebook',font_scale=3)
             mpp.figure(figsize=(16,9))
             from matplotlib.colors import ListedColormap
             featuresSet, targetSet = featuresTrain, targetTrain
             feature1, feature2 = nmp.meshgrid(nmp.arange(start = featuresSet[:, 0].min() - 1,
                                  nmp.arange(start = featuresSet[:, 1].min() - 1, stop = featuresSe
             mpp.contourf(feature1, feature2, classifier.predict(nmp.array([feature1.ravel(), 
                      alpha = 0.6, cmap = ListedColormap(('blue', 'yellow')))
             mpp.xlim(feature1.min(), feature1.max())
             mpp.ylim(feature2.min(), feature2.max())
             for i, j in enumerate(nmp.unique(targetSet)):
                 mpp.scatter(featuresSet[targetSet == j, 0], featuresSet[targetSet == j, 1],
                             c = ListedColormap(('blue', 'yellow'))(i), label = j)
             mpp.title("%s TrainingSet Visual" %(mdel))
             mpp.xlabel('PC 1')
             mpp.ylabel('PC 2')
             mpp.legend()
         def testing_visual(mdel):
             sbn.set_context(context='notebook',font_scale=2)
             mpp.figure(figsize=(16,9))
             from matplotlib.colors import ListedColormap
             featuresSet, targetSet = featuresTest, targetTest
             feature1, feature2 = nmp.meshgrid(nmp.arange(start = featuresSet[:, 0].min() - 1,
                                      nmp.arange(start = featuresSet[:, 1].min() - 1, stop = featu
             mpp.contourf(feature1, feature2, classifier.predict(nmp.array([feature1.ravel(), 
                          alpha = 0.6, cmap = ListedColormap(('blue', 'yellow')))
             mpp.xlim(feature1.min(), feature1.max())
             mpp.ylim(feature2.min(), feature2.max())
             for i, j in enumerate(nmp.unique(targetSet)):
                 mpp.scatter(featuresSet[targetSet == j, 0], featuresSet[targetSet == j, 1],
                             c = ListedColormap(('blue', 'yellow'))(i), label = j)
             mpp.title("%s TestSet Visual" %(mdel))
             mpp.xlabel('PC 1')
             mpp.ylabel('PC 2')
             mpp.legend()
```

13 Function for showing classifier's performance

```
In [39]: from sklearn.model_selection import cross_val_predict, cross_val_score
         from sklearn.metrics import confusion_matrix,classification_report,accuracy_score
         def printScore(classifier,featuresTrain,targetTrain,featuresTest,targetTest,train=True
             if train == True:
                 print("Results_of_training:\n")
                 print('Accuracy_Score: {0:.4f}\n'.format(accuracy_score(targetTrain,classifie
                 print('Classifier_Report:\n{}\n'.format(classification_report(targetTrain,clas
                 print('Confusion_Matrix:\n{}\n'.format(confusion_matrix(targetTrain,classifie
                 res = cross_val_score(classifier, featuresTrain, targetTrain, cv=10, n_jobs=-
                 print('Average_Accuracy:\t{0:.4f}\n'.format(res.mean()))
                 print('Standard_Deviation:\t{0:.4f}'.format(res.std()))
             elif train == False:
                 print("Results_of_testing:\n")
                 print('Accuracy_Score: {0:.4f}\n'.format(accuracy_score(targetTest,classifier
                 print('Classifier_Report:\n{}\n'.format(classification_report(targetTest,clas
                 print('Confusion_Matrix:\n{}\n'.format(confusion_matrix(targetTest,classifier
```

14 ML Classification Algorithms

Now, we are going to apply 2 supervised machine learning algorithms on the mushroom dataset. 1. Support Vector Machine Classifier 2. Naive Bayes Classifier

15 Support Vector Machine Classifier

Support Vector Machine is a supervised machine learning algorithm which can be used for both classification or regression challenges. However, it is mostly used in classification problems. In this algorithm, we plot each data item as a point in n-dimensional space (where n is number of features you have) with the value of each feature being the value of a particular coordinate. Then, we perform classification by finding the hyper-plane that differentiate the two classes very well. Support Vectors are simply the co-ordinates of individual observation. Support Vector Machine is a frontier which best segregates the two classes (hyper-plane/ line).

Advantages

```
1. High-Dimensionality - The SVM is an effective tool in high-dimensional spaces, which is

2. Memory Efficiency - Since only a subset of the training points are used in the actual d

3. Versatility - Class separation is often highly non-linear. The ability to apply new ker
```

Disadvantages

```
1. p>n- In situations where the number of features for each object (p) exceeds the number 

2.Non-Probabilistic - Since the classifier works by placing objects above and below a clas
```

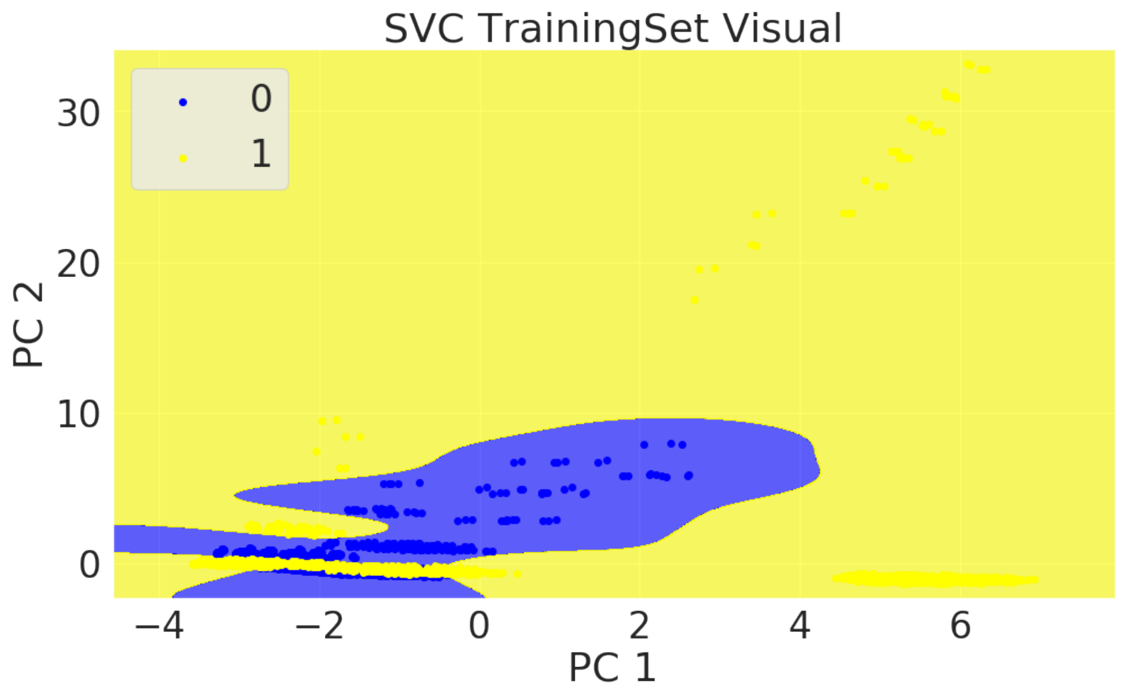
```
In [18]: # Fitting classifier to the mushroom dataset
         from sklearn.svm import SVC
         classifier = SVC(kernel='rbf',random_state=42)
         classifier.fit(featuresTrain,targetTrain)

Out[18]: SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
           decision_function_shape='ovr', degree=3, gamma='auto', kernel='rbf',
           max_iter=-1, probability=False, random_state=42, shrinking=True,
           tol=0.001, verbose=False)

In [40]: printScore(classifier,featuresTrain,targetTrain,featuresTest,targetTest,train=True)
```

```
Results_of_training:

Accuracy_Score: 0.9079

Classifier_Report:
             precision    recall  f1-score   support

          0       0.88      0.99      0.93      2783
          1       0.97      0.78      0.87      1732

avg / total       0.91      0.91      0.91      4515


Confusion_Matrix:
[[2744   39]
 [ 377 1355]]

Average_Accuracy:        0.9072

Standard_Deviation:        0.0108
```

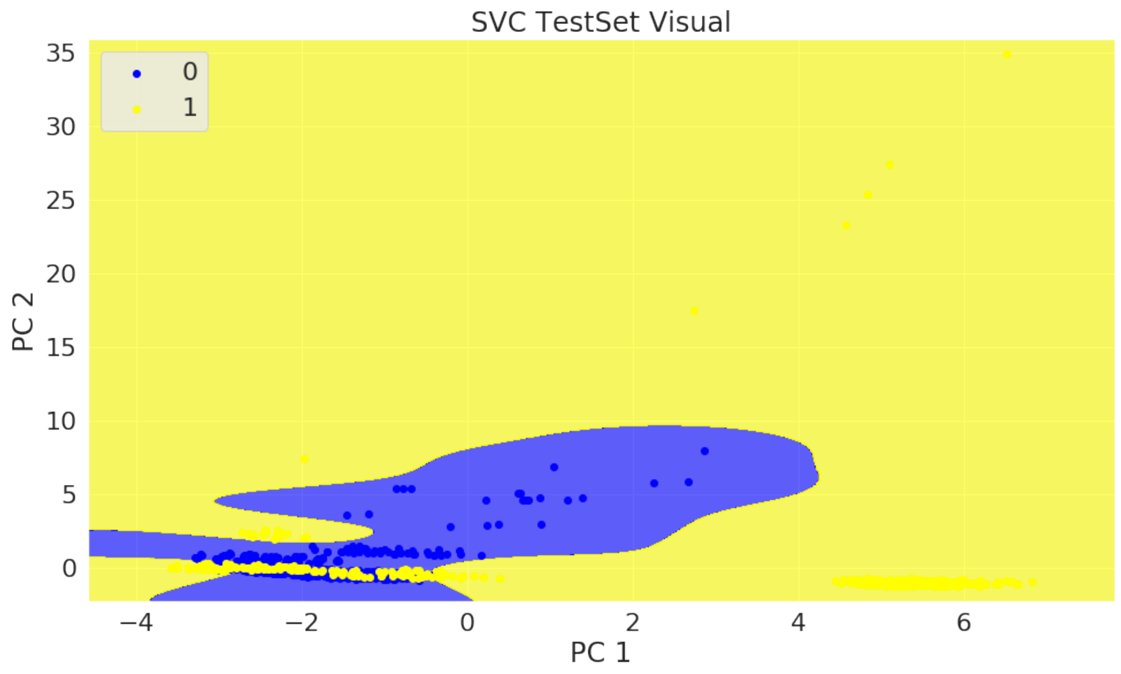
```
In [41]: printScore(classifier,featuresTrain,targetTrain,featuresTest,targetTest,train=False)
```

```
Results_of_testing:

Accuracy_Score: 0.8990

Classifier_Report:
             precision    recall  f1-score   support

          0       0.87      0.99      0.92       705
          1       0.97      0.75      0.85       424

avg / total       0.91      0.90      0.90      1129


Confusion_Matrix:
[[695  10]
 [104 320]]
```

```
In [35]: training_visual('SVC')
```



```
In [36]: testing_visual('SVC')
```



16 Naive Bayes Classifier

Naive Bayes is a kind of classifier which uses the Bayes Theorem. It predicts membership probabilities for each class such as the probability that given record or data point belongs to a particular class. The class with the highest probability is considered as the most likely class. This is also known as Maximum A Posteriori (MAP).

The MAP for a hypothesis is:

MAP(H) = max(P(H|E)) = max((P(E|H)*P(H))/P(E)) = max(P(E|H)*P(H))

P(E) is evidence probability, and it is used to normalize the result. It remains same so, removing it won't affect.

Naive Bayes classifier assumes that all the features are unrelated to each other. Presence or absence of a feature does not influence the presence or absence of any other feature.

```
In [37]: # Fitting classifier to the mushroom dataset
         from sklearn.naive_bayes import GaussianNB as NB
         clas = NB()
         clas.fit(featuresTrain,targetTrain)

Out[37]: GaussianNB(priors=None)

In [43]: printScore(clas,featuresTrain,targetTrain,featuresTest,targetTest,train=True)
```

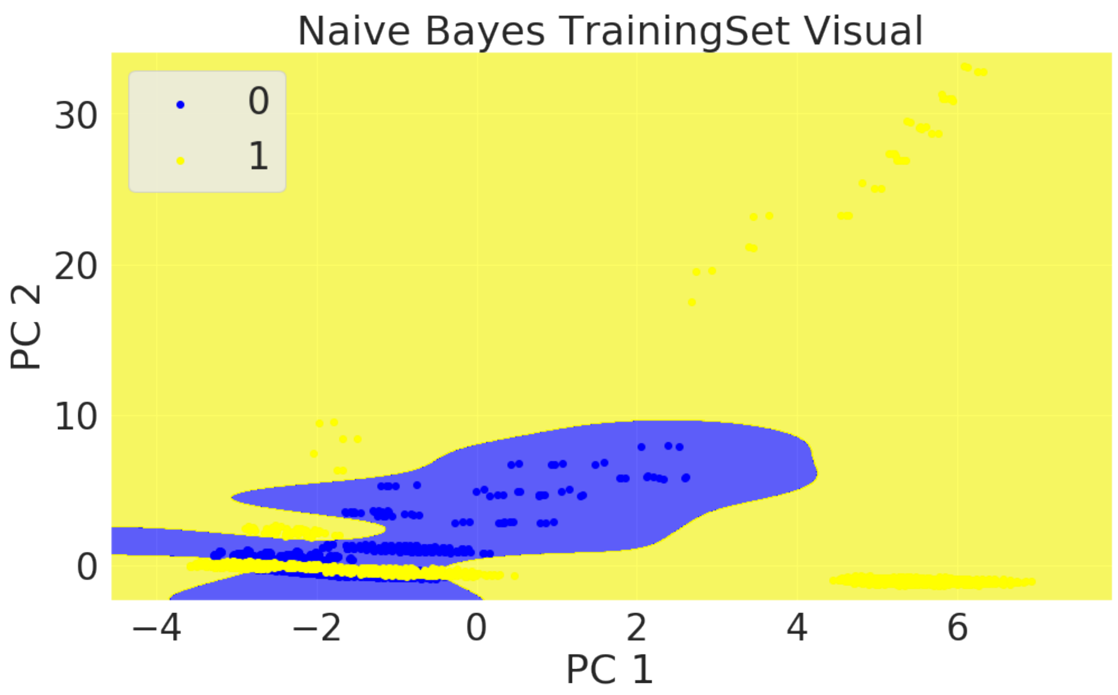
```
Results_of_training:

Accuracy_Score: 0.8443

Classifier_Report:
             precision    recall  f1-score   support

          0       0.81      0.97      0.89      2783
          1       0.94      0.64      0.76      1732

avg / total       0.86      0.84      0.84      4515


Confusion_Matrix:
[[2708   75]
 [ 628 1104]]

Average_Accuracy:        0.8443

Standard_Deviation:        0.0165
```

```
In [44]: printScore(clas,featuresTrain,targetTrain,featuresTest,targetTest,train=False)
```

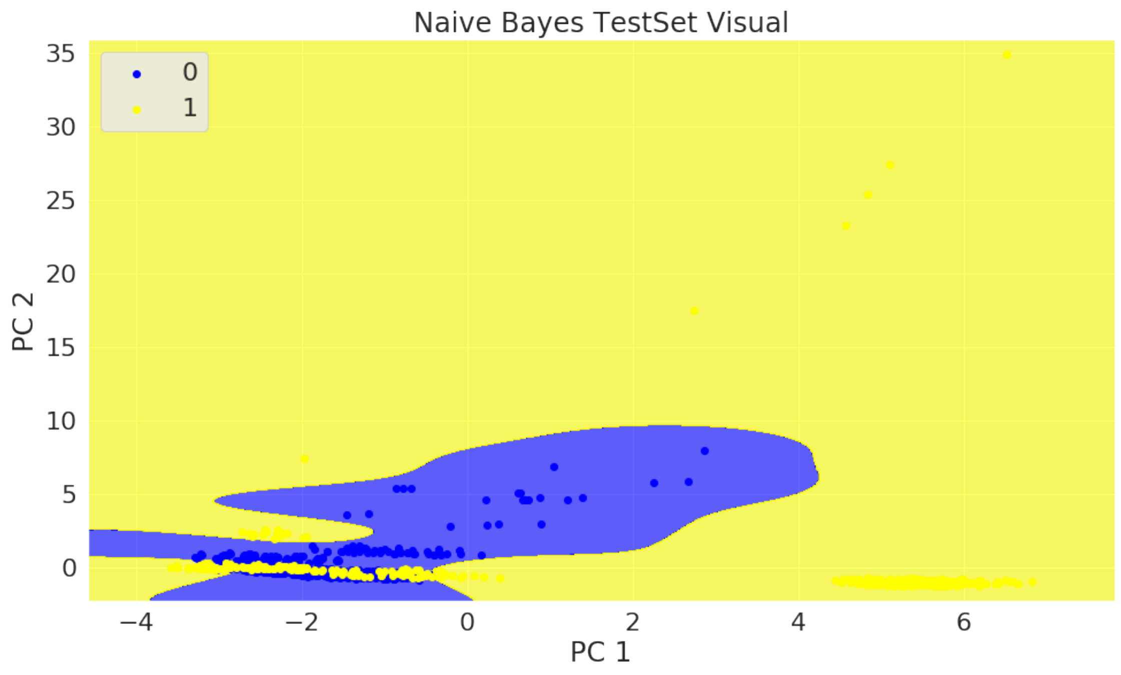
```
Results_of_testing:

Accuracy_Score: 0.8299
```

```
Classifier_Report:
             precision    recall  f1-score   support

          0       0.80      0.97      0.88       705
          1       0.92      0.60      0.73       424

avg / total       0.84      0.83      0.82      1129


Confusion_Matrix:
[[682  23]
 [169 255]]
```

```
In [45]: training_visual('Naive Bayes')
```



```
In [47]: testing_visual('Naive Bayes')
```


Naive Bayes TestSet Visual
0
1
PC 2
PC 1
35
30
25
20
15
10
5
0
−4
−2
0
2
4
6

```
In [ ]:
```