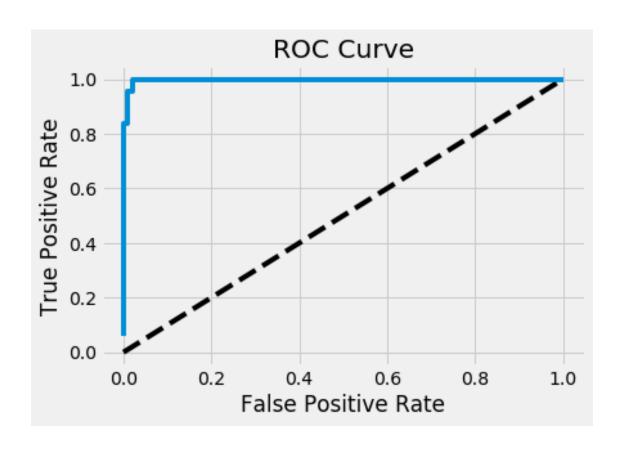
## Untitled3

## May 19, 2019

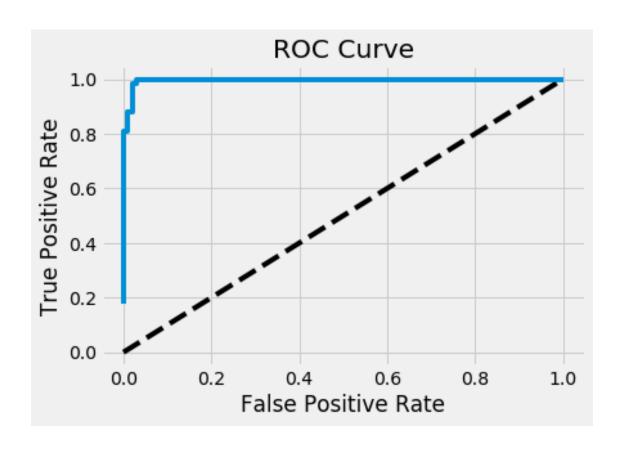
```
In [6]: # for basic operations
        import numpy as np
        import pandas as pd
        # data visualization
        import matplotlib.pyplot as plt
        import seaborn as sns
        plt.style.use('fivethirtyeight')
        data = pd.read_csv('C:/Users/Kai/Desktop/Assignment3/data/breast-w_preproccess.csv')
        # for basic operations
        import numpy as np
        import pandas as pd
        # data visualization
        import matplotlib.pyplot as plt
        import seaborn as sns
        plt.style.use('fivethirtyeight')
        data = pd.read_csv('C:/Users/Kai/Desktop/Assignment3/data/breast-w_preproccess.csv')
        data.head(6)
Out[6]:
           Clump_Thickness
                           Cell_Size_Uniformity Cell_Shape_Uniformity \
        0
                         5
                                                                        1
                         5
        1
                                                                        4
        2
                         3
                                                1
                                                                        1
        3
                         6
                                                8
                                                                        8
        4
                         4
                                                1
                                                                        1
        5
                         8
                                               10
                                                                       10
           Marginal_Adhesion
                              Single_Epi_Cell_Size
                                                    Bare_Nuclei Bland_Chromatin
        0
                                                                1
                           5
                                                  7
        1
                                                              10
                                                                                 3
        2
                           1
                                                  2
                                                                2
                                                                                 3
        3
                           1
                                                  3
                                                                4
                                                                                 3
```

```
7
        5
                            8
                                                                 10
                                                                                    9
           Normal_Nucleoli
                            Mitoses
                                           Class
        0
                                          benign
                          1
        1
                          2
                                    1
                                          benign
        2
                          1
                                    1
                                          benign
                          7
        3
                                          benign
        4
                          1
                                    1
                                          benign
        5
                                       malignant
In [21]: def one_hot_encoder(df, nan_as_category = False):
             original_columns = list(df.columns)
              categorical_columns = [col for col in df.columns if df[col].dtype == 'object']
              df = pd.get_dummies(df, columns= categorical_columns, dummy_na= nan_as_category,
             new_columns = [c for c in df.columns if c not in original_columns]
             return df, new_columns
         data, new_columns = one_hot_encoder(data)
         data.head(6)
Out [21]:
            Clump_Thickness Cell_Size_Uniformity Cell_Shape_Uniformity
         0
                           5
                           5
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                                                   4
                                                                            4
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                                                                            1
         3
                           6
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                           4
                                                   1
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         5
                           8
                                                  10
                                                                           10
            Marginal_Adhesion Single_Epi_Cell_Size
                                                        Bare_Nuclei Bland_Chromatin \
         0
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                                                                                     3
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         2
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                                                     3
                                                                                     3
         3
                              1
                                                                   4
                                                     2
                                                                                     3
         4
                              3
                                                                   1
                                                     7
         5
                                                                  10
                                                                                     9
            Normal_Nucleoli Mitoses
                                        Class_malignant
         0
                                                       0
                           2
                                     1
                                                       0
         1
         2
                           1
                                     1
                                                       0
         3
                           7
                                     1
                                                       0
         4
                           1
                                     1
                                                       0
         5
                           7
                                     1
                                                       1
```

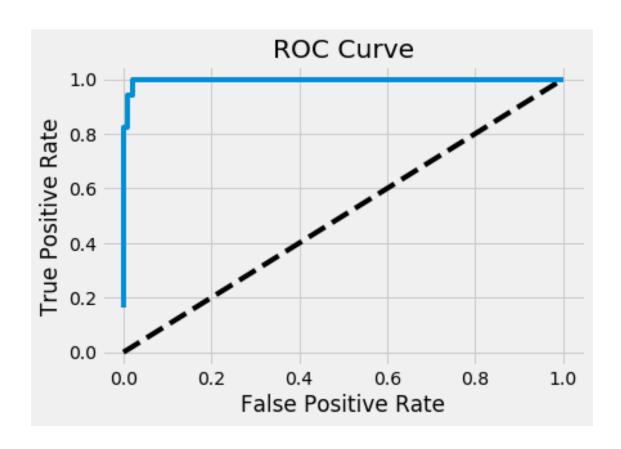
```
y = data["Class_malignant"].values
         # Spliting X and y into train and test version
         X_train, X_test, y_train, y_test = train_test_split(x, y, test_size = 0.25, random_st
In [43]: from sklearn import neighbors
         from sklearn.ensemble import BaggingRegressor
         from sklearn.metrics import r2_score
         from sklearn.utils import resample
         from sklearn.metrics import roc_curve
         def KNeighborsBagging(neigh):
             kn1= neighbors.KNeighborsRegressor(n_neighbors=neigh, weights='uniform')
             kn2= neighbors.KNeighborsRegressor(n_neighbors=neigh,weights='distance')
             bgg= BaggingRegressor(kn1,n_estimators=10,max_samples=0.7,max_features=0.9,verbos
             bgg.fit(X_train, y_train)
             print(bgg.score(X_train, y_train))
             y_pred = bgg.predict(X_test)
             # Generate ROC curve values: fpr, tpr, thresholds
             fpr, tpr, thresholds = roc_curve(y_test, y_pred)
             # Plot ROC curve
             plt.plot([0, 1], [0, 1], 'k--')
             plt.plot(fpr, tpr)
             plt.xlabel('False Positive Rate')
             plt.ylabel('True Positive Rate')
             plt.title('ROC Curve')
             plt.show()
In [55]: KNeighborsBagging(30)
```



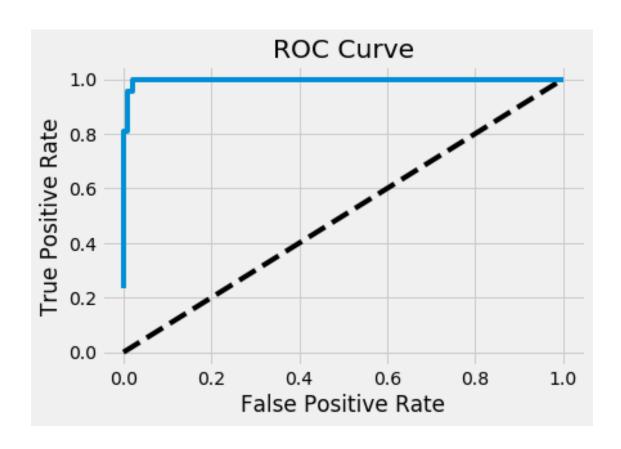
In [54]: KNeighborsBagging(20)



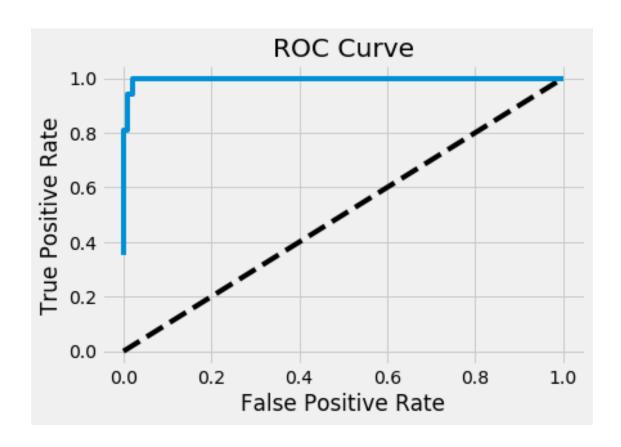
In [53]: KNeighborsBagging(15)



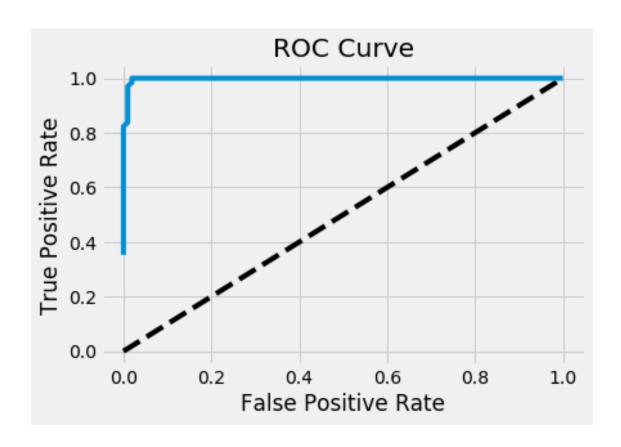
In [44]: KNeighborsBagging(10)



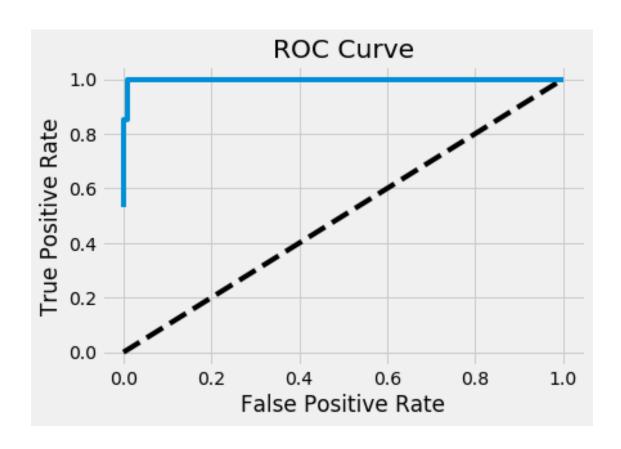
In [48]: KNeighborsBagging(8)



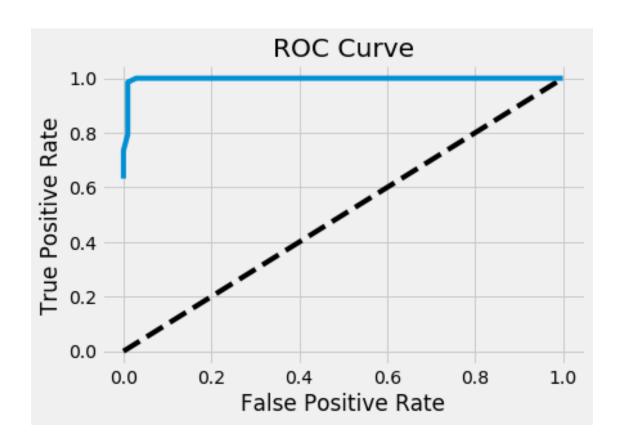
In [49]: KNeighborsBagging(6)



In [50]: KNeighborsBagging(3)



In [51]: KNeighborsBagging(2)



In [52]: KNeighborsBagging(1)

