Hands-on Exercise CLASS Module

In [1]: #!pip install --user mlxtend In [2]: import numpy as np import pandas as pd #Plotting packages import matplotlib.pyplot as plt import seaborn as sns #Classification Algorithms from sklearn.tree import DecisionTreeClassifier from sklearn.neighbors import KNeighborsClassifier from sklearn.naive bayes import GaussianNB from sklearn.svm import SVC #Ensemble Methods from sklearn.ensemble import BaggingClassifier from sklearn.ensemble import BaggingRegressor from sklearn.model_selection import cross_val_score, train_test_split from sklearn.ensemble import AdaBoostClassifier In [3]: #MLxtend for visualizing classification decision boundaries from mlxtend.plotting import plot decision regions

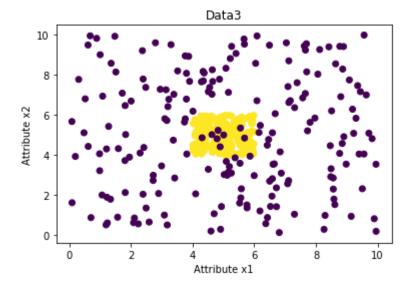
```
In [4]: # Generating Data1
        np.random.seed(100)
        a = np.random.multivariate_normal([2,2],[[0.5,0], [0,0.5]], 200)
        b = np.random.multivariate_normal([4,4],[[0.5,0], [0,0.5]], 200)
        Data1 X = np.vstack((a,b))
        Data1 Y = np.hstack((np.ones(200).T,np.zeros(200).T)).astype(int)
        # Generating Data2
        np.random.seed(100)
        a1 = np.random.multivariate_normal([2,2],[[0.25,0], [0,0.25]],200)
        a2 = np.random.multivariate_normal([2,4],[[0.25,0], [0,0.25]],200)
        a3 = np.random.multivariate_normal([4,2],[[0.25,0], [0,0.25]],200)
        a4 = np.random.multivariate_normal([4,4],[[0.25,0], [0,0.25]],200)
        Data2 X = np.vstack((a1,a4,a2,a3))
        Data2_Y = np.hstack((np.ones(400).T,np.zeros(400).T)).astype(int)
        # Generating Data3
        np.random.seed(100)
        a1 = np.random.uniform(4,6,[200,2])
        a2 = np.random.uniform(0,10,[200,2])
        Data3 X = np.vstack((a1,a2))
        Data3 Y = np.hstack((np.ones(200).T,np.zeros(200).T)).astype(int)
        # Generating Data4
        np.random.seed(100)
        Data4 X = np.random.uniform(0,12,[500,2])
        Data4_Y = np.ones([500]).astype(int)
        Data4_Y[np.multiply(Data4_X[:,0],Data4_X[:,0]) + np.multiply(Data4_X[:,1],Data
        4_X[:,1]) - 100 < 0 ] = 0
```

1. Decision Tree

Use **Data3** to answer the following questions.

^{**}Question 1a:** Compute and print the 10-fold cross-validation accuracy using decision tree classifiers with max_depth = 2,4,6,8,10, and 50.

```
In [5]: import matplotlib.pyplot as plt
   plt.scatter(Data3_X[:,0],Data3_X[:,1], c=Data3_Y)
   plt.xlabel('Attribute x1')
   plt.ylabel('Attribute x2')
   plt.title('Data3')
   plt.show()
```



```
In [6]: dt2 = DecisionTreeClassifier(max_depth=2)
    dt4 = DecisionTreeClassifier(max_depth=4)
    dt6 = DecisionTreeClassifier(max_depth=6)
    dt8 = DecisionTreeClassifier(max_depth=8)
    dt10 = DecisionTreeClassifier(max_depth=10)
    dt50 = DecisionTreeClassifier(max_depth=50)
```

```
In [7]: dt2_score = cross_val_score(dt2, Data3_X, Data3_Y, cv=10, scoring='accuracy')
    dt4_score = cross_val_score(dt4, Data3_X, Data3_Y, cv=10, scoring='accuracy')
    dt6_score = cross_val_score(dt6, Data3_X, Data3_Y, cv=10, scoring='accuracy')
    dt8_score = cross_val_score(dt8, Data3_X, Data3_Y, cv=10, scoring='accuracy')
    dt10_score = cross_val_score(dt10, Data3_X, Data3_Y, cv=10, scoring='accuracy')
    dt50_score = cross_val_score(dt50, Data3_X, Data3_Y, cv=10, scoring='accuracy')
```

```
Depth
           Score
0
          0.8750
       2
1
       4
          0.9700
2
         0.9675
       6
3
       8
          0.9500
4
      10
          0.9425
      50
          0.9450
```

Question 1b: For what values of max_depth did you observe the lowest accuracy? What is this phenomenon called?

```
In [9]: print(dt_accuracy_df.loc[dt_accuracy_df.Score.idxmin()])

Depth    2.000
    Score    0.875
    Name: 0, dtype: float64
```

Answer: For max depth = 2. The accuracy was the lowest. This phenomenon is called underfitting

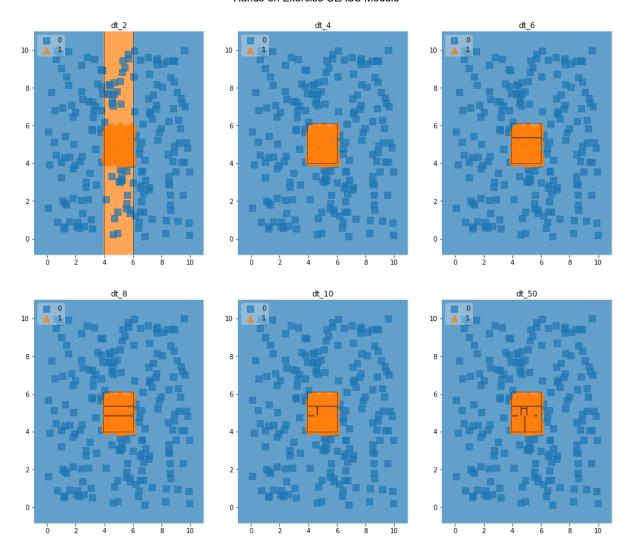
Question 1c: What accuracy did you observe for max depth=50? What is the difference between this accuracy and the highest accuracy? What is this phenomenon called?

```
dt_accuracy_df.loc[dt_accuracy_df['Depth'] == 50.000]['Score']
In [10]:
Out[10]: 5
              0.945
         Name: Score, dtype: float64
In [11]:
          dt accuracy df.loc[dt accuracy df.Score.idxmax()]
Out[11]: Depth
                  4.00
         Score
                  0.97
         Name: 1, dtype: float64
         dt_accuracy_df.loc[dt_accuracy_df.Score.idxmax()]['Score'] - dt_accuracy_df.lo
In [12]:
         c[dt accuracy df['Depth'] == 50.000]['Score']
Out[12]: 5
              0.025
         Name: Score, dtype: float64
```

**Answer: ** Accuracy for Max depth 50 is 94.5% whereas the highest accuracy is 97% for maxdepth = 4. The decrease in accuracy is due to overfitting

Question 1d: Plot decision regions for the above decision tree models

```
In [13]: # parameters to set size or markers, contours, and transparency
         scatter_kwargs = {'s': 120, 'edgecolor': None, 'alpha': 0.7}
         contourf_kwargs = {'alpha': 0.7}
         scatter highlight kwargs = {'s': 120, 'label': 'Test data', 'alpha': 0.7}
         # Creating a list of classifiers and their names for plotting
         clf list = [dt2, dt4, dt6, dt8, dt10, dt50]
         labels = ['dt_2','dt_4','dt_6','dt_8','dt_10','dt_50']
         # Plotting the decision boundaries
         fig = plt.figure(figsize=(16,14))
         count = 0;
         for clf, label in zip(clf_list, labels):
             count = count + 1;
             clf.fit(Data3_X, Data3_Y)
             ax = plt.subplot(2,3,count)
             fig = plot_decision_regions(X=Data3_X, y=Data3_Y, clf=clf, legend=2,
                                  scatter kwargs=scatter kwargs,
                                  contourf kwargs=contourf kwargs,
                                  scatter_highlight_kwargs=scatter_highlight_kwargs)
             plt.title(label)
         plt.show()
```



Question 1e: Based on the decision regions, which depth is better suited for this data? Explain your reason.

Answer: Maxdepth 4 is the better suited for the data based on decision regions, this would only misclassify 0's in the center

- · Depth2: Too many 0's wrongly classified as 1's. This is an underfitting model
- Depth6: Creates 2 region in the center which wrongly classifies some of the 1's as 0's due to the presence of 0's in the central region, thus increasing the misclassification
- Depth8: Creates 3 new region in the center which wrongly classifies some of the 1's as 0's due to the presence of 0's in the central region, thus increasing the misclassification
- Depth10: Creates 5 regions in the center which wrongly classifies some of the 1's as 0's due to the presence of 0's in the central region, thus increasing the misclassification
- Depth50: Creates 7 regions in the center to account for the presence of 0's in the central region, thus
 increasing the misclassification. This is an example of overfitting model

2. k Nearest Neighbor

Use **Data2** to answer the following questions.

Question 2a: Compute and print the 10-fold cross-validation accuracy for a kNN classifier with n_neighbors = 1, 5, 10, 50

```
In [14]: knn1 = KNeighborsClassifier(n_neighbors=1)
    knn5 = KNeighborsClassifier(n_neighbors=5)
    knn10 = KNeighborsClassifier(n_neighbors=10)
    knn50 = KNeighborsClassifier(n_neighbors=50)
```

```
In [15]: knn1_score = cross_val_score(knn1, Data2_X, Data2_Y, cv=10, scoring='accuracy'
) knn5_score = cross_val_score(knn5, Data2_X, Data2_Y, cv=10, scoring='accuracy'
) knn10_score = cross_val_score(knn10, Data2_X, Data2_Y, cv=10, scoring='accuracy')
knn50_score = cross_val_score(knn50, Data2_X, Data2_Y, cv=10, scoring='accuracy')
```

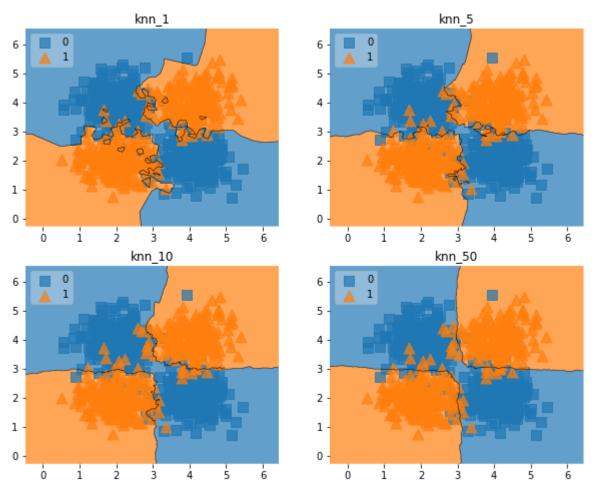
```
Neighbours Score
0 1 0.91250
1 5 0.93500
2 10 0.94000
3 50 0.94125
```

Question 2b: For what values of n_neighbors did you observe the lowest accuracy? What is this phenomenon called?

Answer: Neighbour 1 has the lowest accuracy. This phenomenon is called overfitting

Question 2c: Plot decision regions for a kNN classifier with n neighbors = 1, 5, 10, 50

```
In [18]: # Creating a list of classifiers and their names for plotting
         clf list = [knn1,knn5,knn10,knn50]
         labels = ['knn_1','knn_5','knn_10','knn_50']
         # Plotting the decision boundaries
         fig = plt.figure(figsize=(10,8))
         count = 0;
         for clf, label in zip(clf_list, labels):
             count = count + 1;
             clf.fit(Data2_X, Data2_Y)
             ax = plt.subplot(2,2,count)
             fig = plot_decision_regions(X=Data2_X, y=Data2_Y, clf=clf, legend=2,
                                  scatter_kwargs=scatter_kwargs,
                                  contourf kwargs=contourf kwargs,
                                  scatter_highlight_kwargs=scatter_highlight_kwargs)
             plt.title(label)
         plt.show()
```



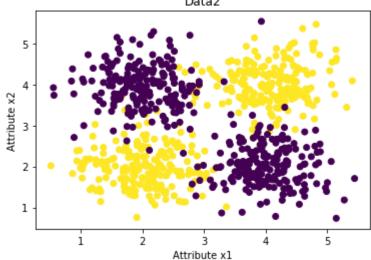
Question 2d: From the plots for **Question 2c** what do you notice about the nature of decision boundary as the n_neighbors are increasing.

Answer: As neighbours are increasing the decision region is becoming more and more generalized.

3. Naive Bayes

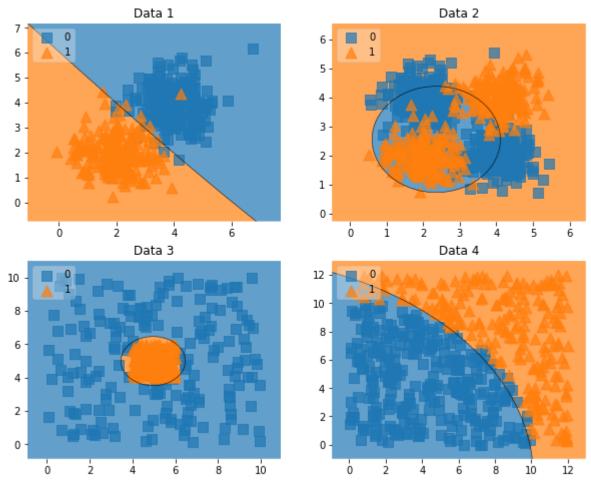
Question 3a: Compute and print the 10-fold cross-validation accuracy for a NB classifier on all four datasets: Data1, Data2, Data3, Data4

```
In [19]: nb = GaussianNB()
         nb_scores_1 = cross_val_score(nb, Data1_X, Data1_Y, cv=10, scoring='accuracy')
In [20]:
         nb_scores_2 = cross_val_score(nb, Data2_X, Data2_Y, cv=10, scoring='accuracy')
         nb_scores_3 = cross_val_score(nb, Data3_X, Data3_Y, cv=10, scoring='accuracy')
         nb_scores_4 = cross_val_score(nb, Data4_X, Data4_Y, cv=10, scoring='accuracy')
In [21]: nb_accuracy_df = pd.DataFrame.from_dict({ 'Dataset': [1,2,3,4],
              'Score': [nb_scores_1.mean(),nb_scores_2.mean(),nb_scores_3.mean(),nb_scor
         es 4.mean()]})
         print(nb accuracy df)
            Dataset
                        Score
         0
                     0.967500
         1
                  2 0.050000
         2
                  3 0.960000
                  4 0.964074
         plt.scatter(Data2_X[:,0],Data2_X[:,1], c= Data2_Y)
In [22]:
         plt.xlabel('Attribute x1')
         plt.ylabel('Attribute x2')
         plt.title('Data2')
         plt.show()
                                  Data2
            5
```



- **Question 3b:** State your observations on the datasets the NB algorithm performed poorly.
- **Answer:** As we know naive bayes forms a distribution for a class based on the training points, in the above case the ditributions for each class will overlap with one another, leading to low accuracy.
- **Question 3c:** Plot decision regions for a NB classifier on each of the four datasets

```
In [23]: # Creating a list of classifiers and their names for plotting
         data list = [Data1 X,Data2 X,Data3 X,Data4 X]
         label_list = [Data1_Y,Data2_Y,Data3_Y, Data4_Y]
         labels = ['Data 1','Data 2','Data 3','Data 4']
         # Plotting the decision boundaries
         fig = plt.figure(figsize=(10,8))
         count = 0;
         for X, y, label in zip(data_list, label_list, labels):
             count = count + 1;
             nb.fit(X, y)
             ax = plt.subplot(2,2,count)
             fig = plot_decision_regions(X=X, y=y, clf=nb, legend=2,
                                  scatter_kwargs=scatter_kwargs,
                                  contourf kwargs=contourf kwargs,
                                  scatter_highlight_kwargs=scatter_highlight_kwargs)
             plt.title(label)
         plt.show()
```



Question 3d: Describe the shape of the decision boundary on all four datasets. Explain the reason.

**Answer:

- 1. Linear
- 2. Ellipsoidal
- 3. Ellipsoidal
- 4. curve

4. Support Vector Machines (Linear)

Question 4a: Based on the visualization of the four datasets, assess how well a linear SVM is expected to perform. Specifically, rank the datasets in the order of decreasing accuracy when a linear SVM is used. No need to compute accuracy to answer this question.

```
**Answer:** 1. D1, 2. D4, 3. D3, 4.D2
```

Question 4b: Compute and print the 10-fold cross-validation accuracy for a linear SVM classifier on all four datasets: Data1, Data2, Data3, Data4

```
In [24]: svm_linear = SVC(C=0.5, kernel='linear')
In [25]: svm_scores_1 = cross_val_score(svm_linear, Data1_X, Data1_Y, cv=10, scoring='a ccuracy')
    svm_scores_2 = cross_val_score(svm_linear, Data2_X, Data2_Y, cv=10, scoring='a ccuracy')
    svm_scores_3 = cross_val_score(svm_linear, Data3_X, Data3_Y, cv=10, scoring='a ccuracy')
    svm_scores_4 = cross_val_score(svm_linear, Data4_X, Data4_Y, cv=10, scoring='a ccuracy')
```

^{**} Actually there're no decision regions per se, the points when classified to a class changes to the color of that class based on it's probability, which when seen cumulatively appears as a region. In general Naive Bayes only provides with the probability of a class given a point label based on it's distribution

^{**}Question 3e:** Based on your plots in Question 3c explain the poor performance of NB on some datasets.

^{**}Answer: NB performs well when the data from different classes are well seperated meaning the distribution for the classes has zero to little overlap, if there is some overlap between the distribution of the classes, the performance of NB classifier suffers**

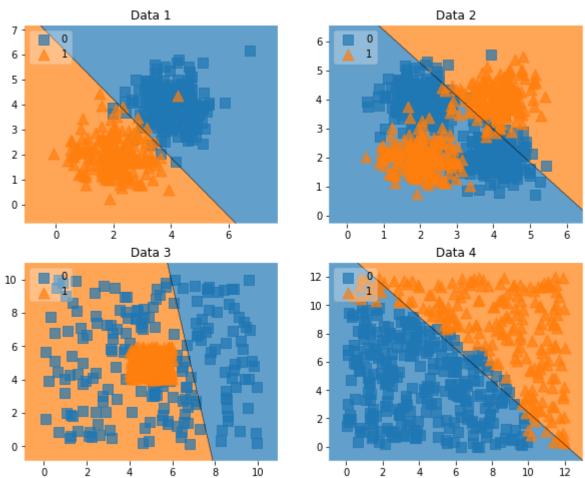
```
Dataset Score
0 1 0.967500
1 2 0.141250
2 3 0.642500
3 4 0.925946
```

^{**}Question 4c:** Rank the datasets in the decreasing order of accuracy of SVM.

^{**}Answer:** 1. D1, 2. D4, 3. D3, 4.D2

^{**}Question 4d:** Plot decision regions for a linear SVM classifier on each of the four datasets

```
In [27]: # Creating a list of classifiers and their names for plotting
         data list = [Data1 X,Data2 X,Data3 X,Data4 X]
         label_list = [Data1_Y,Data2_Y,Data3_Y, Data4_Y]
         labels = ['Data 1','Data 2','Data 3','Data 4']
         # Plotting the decision boundaries
         fig = plt.figure(figsize=(10,8))
         count = 0;
         for X, y, label in zip(data_list, label_list, labels):
             count = count + 1;
             svm_linear.fit(X, y)
             ax = plt.subplot(2,2,count)
             fig = plot_decision_regions(X=X, y=y, clf=svm_linear, legend=2,
                                  scatter_kwargs=scatter_kwargs,
                                  contourf kwargs=contourf kwargs,
                                  scatter_highlight_kwargs=scatter_highlight_kwargs)
             plt.title(label)
         plt.show()
```



Question 4e. Explain the reason for your observations in **Question 4c** using observations from the above decision regions.

Answer: As we can see from the above plots, svm is able to do a clearer seperation on D1 compared to D2, where SVM fairs better than D4, for which svm although looks to have failed miserbaly is still better than SVM Linear classification on D3

5. Non-linear Support Vector Machines

Use **Data2** to answer the following questions.

Question 5a: Compute and print the 10-fold cross-validation accuracy for an SVM with a polynomial kernel and degree values 1, 2, and 3.

```
In [28]: svm_poly = SVC(C=0.5, kernel='poly',degree=1, gamma = 'auto')
    svm_poly_2 = SVC(C=0.5, kernel='poly',degree=2, gamma = 'auto')
    svm_poly_3 = SVC(C=0.5, kernel='poly',degree=3, gamma = 'auto')

In [29]: svm_poly_scores = cross_val_score(svm_poly, Data2_X, Data2_Y, cv=10, scoring= 'accuracy')
```

```
'accuracy')

svm_poly_scores_2 = cross_val_score(svm_poly_2, Data2_X, Data2_Y, cv=10, scoring=

ng='accuracy')

svm_poly_scores_3 = cross_val_score(svm_poly_3, Data2_X, Data2_Y, cv=10, scoring=

ng='accuracy')
```

Question 5b: Rank the polynomial kernels in decreasing order of accuracy.

^{**}Answer: Degree 3, Degree 2 and Degree 1**

^{**}Question 5c:** Plot decision regions for a polynomial kernel SVM with degree values 1, 2, and 3.

```
In [31]: # Creating a list of classifiers and their names for plotting
         clf list = [svm poly,svm poly 2,svm poly 3]
         labels = ['Deg_1','Deg_2','Deg_3']
         # Plotting the decision boundaries
         fig = plt.figure(figsize=(20,5))
         count = 0;
         for clf, label in zip(clf_list, labels):
             count = count + 1;
             clf.fit(Data2 X, Data2 Y)
             ax = plt.subplot(1,3,count)
             fig = plot_decision_regions(X=Data2_X, y=Data2_Y, clf=clf, legend=2,
                                  scatter kwargs=scatter kwargs,
                                  contourf kwargs=contourf kwargs,
                                  scatter_highlight_kwargs=scatter_highlight_kwargs)
             plt.title(label)
         plt.show()
                     Deg 1
                                                 Deg_2
```

Question 5d: Based on the decision regions, explain the reason for your observations in **Question 5c**.

Answer: SVM with degree 1 is a linear separator trying to separate linearly unseparable data hence it fails miserably. SVM with degree 2 perfoms better as it uses 2 linear separators to chart out a region for class 1. SVM with degree 3 performs even better because it uses curves to further refine the decision region

Question 5e: Compute the 10-fold cross-validation accuracy for an SVM with an RBF kernel and gamma values 0.01, 0.1, and 1.

```
In [32]: svm_rbf_001 = SVC(C = 0.5, kernel='rbf', gamma=0.01)
    svm_rbf_01 = SVC(C = 0.5, kernel='rbf', gamma=0.1)
    svm_rbf_1 = SVC(C = 0.5, kernel='rbf', gamma=1)
```

Question 5g: Plot decision regions for the above RBF Kernels

```
In [35]:
         # Creating a list of classifiers and their names for plotting
         clf_list = [svm_rbf_001,svm_rbf_01,svm_rbf_1]
         labels = ['rbf_001','rbf_01','rbf_1']
         # Plotting the decision boundaries
         fig = plt.figure(figsize=(20,5))
         count = 0;
         for clf, label in zip(clf_list, labels):
             count = count + 1;
             clf.fit(Data2_X, Data2_Y)
             ax = plt.subplot(1,3,count)
             fig = plot decision regions(X=Data2 X, y=Data2 Y, clf=clf, legend=2,
                                  scatter kwargs=scatter kwargs,
                                  contourf_kwargs=contourf_kwargs,
                                  scatter highlight kwargs=scatter highlight kwargs)
             plt.title(label)
         plt.show()
```

^{**}Question 5f:** Rank the RBF kernels in decreasing order of accuracy.

^{**}Answer: 1. svm_rbf_scores_1, 2. svm_rbf_scores_01, 3.svm_rbf_scores_001**

^{**}Question 5h:** Explain the reason for your observations in **Question 5f** from the above decision regions.

Answer: 1. svm_rbf_.001 performs very badly because we tell the kernel that the variance between the points is very high and hence the rbf tries to account for it. 2. svm_rbf_.01 performs very well better because the variance set for the kernel appropriates the variance in the data 3. svm_rbf_1 also performs very well, infact marginally better than svm_rbf_1 because the decrease in variance fits the data better

Question 5i: Between SVM with a Polynomial kernel and SVM with an RBF kernel, which one is ideally suited of Data3? Explain your reason.

Answer: svm_rbf_1 (i.e. gamma = 1) is better suited because it covers the pattern of points very well

6. Classification Evaluation

Question 6a:

Run SVM classifier (with RBF kernel and gamma=0.1) on **Data2** and compute the mean of k-fold cross-validation accuracies for cv = 3, 4, 5 and 6. Report the mean of accuracies for each choice of 'cv' and explain the reason for any differences in the mean accuracy you observe.

```
Order Score
0 cv_3 0.903827
1 cv_4 0.916250
2 cv_5 0.927500
3 cv_6 0.932553
```

Answer: This may be due to the increase in training data points the more the data points used to trained the model, the better the model accuracy

Question 6b:

For DT, NB, kNN, Linear SVM, Polynomial Kernel SVM, and SVM with RBF kernel classifiers, compute the 30-fold crossvalidation **accuracies** and **precision** (use scoring='precision' when calling cross_val_score()) on **Data3**. Rank the classifiers based on accuracy and precision scores. Are the best classifiers ranked according to accuracy and precision the same? If not, explain the reason.

For the classifiers, feel free to choose any parameter settings you prefer.

```
In [38]: dt4_accuracy_score = cross_val_score(dt4, Data3_X, Data3_Y, cv=30, scoring='accuracy')
    nb_accuracy_score = cross_val_score(nb, Data3_X, Data3_Y, cv=30, scoring='accuracy')
    knn5_accuracy_score = cross_val_score(knn5, Data3_X, Data3_Y, cv=30, scoring='accuracy')
    svm_linear_accuracy_score = cross_val_score(svm_linear, Data3_X, Data3_Y, cv=30, scoring='accuracy')
    svm_poly_accuracy_score = cross_val_score(svm_poly_3, Data3_X, Data3_Y, cv=30, scoring='accuracy')
    svm_rbf_accuracy_score = cross_val_score(svm_rbf_1, Data3_X, Data3_Y, cv=30, scoring='accuracy')
```

```
Classifier Score

0 dt 0.971825

1 nb 0.959127

2 knn 0.949206

3 svm_linear 0.642857

4 svm_poly 0.855556

5 svm_rbf 0.954365
```

```
Classifier Score

dt 0.971825

nb 0.959127

knn 0.949206

svm_linear 0.642857

svm_poly 0.855556

svm rbf 0.954365
```

7. Ensemble Methods

Question 7a: **Bagging:** Create bagging classifiers each with n_estimators = 1,2,3,4,5,10, and 20. Use a **linear SVM** (with C=0.5) as a base classifier. Using **Data3**, compute the mean **5-fold** cross validation accuracies and standard deviation for each of the bagging classifiers. State your observations on how bagging affected the mean and standard deviation of the base classifier. Explain your reason for what may have lead to these observations.

```
n est list = [1,2,3,4,5,10,20]
In [42]:
         for n est in n est list:
             # create an instance of bagging classifier with 'n est' estimators
             bagging = BaggingClassifier(base estimator=svm linear, n estimators=n est)
             # compute cross-validation accuracy for each bagging classifier
             scores = cross_val_score(bagging, Data3_X, Data3_Y, cv=5, scoring='accurac
         y')
             print("Bagging Accuracy: %.2f (+/- %.2f) #estimators: %d" % (scores.mean
         (), scores.std(), n_est))
         Bagging Accuracy: 0.58 (+/- 0.07) #estimators: 1
         Bagging Accuracy: 0.57 (+/- 0.08) #estimators: 2
         Bagging Accuracy: 0.64 (+/- 0.04) #estimators: 3
         Bagging Accuracy: 0.59 (+/- 0.08) #estimators: 4
         Bagging Accuracy: 0.62 (+/- 0.04) #estimators: 5
         Bagging Accuracy: 0.75 (+/- 0.11) #estimators: 10
         Bagging Accuracy: 0.68 (+/- 0.07) #estimators: 20
```

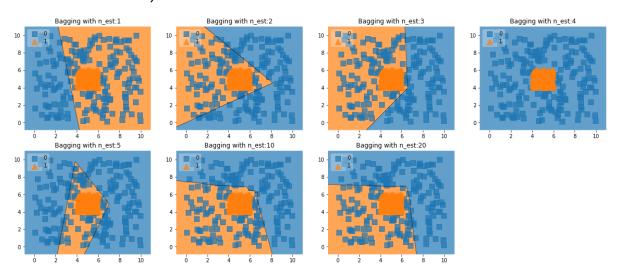
^{**}Answer: Yes in both cases decision tree with max depth = 4 is the best classifier**

Answer: Accuracy Mean and SD is almost same for estimators 1,2 and 4. Esimators 3 and 4 are also interms of SD and Mean. Bagging with 10 estimators show the highest accuracy and higher standar deviation suggesting that although the mean accuracy is high the spread of the accuracy is large compared to other estimators. Bagging with 20 estimators have mean accuracy and sd little less compared to estimator 20, suggesting the effect of some kind of overfitting of training data on the model

Question 7b: Plot decision regions for the above bagging classifiers.

/users/PES0801/nifaullah/.local/lib/python3.6/site-packages/mlxtend/plotting/decision_regions.py:247: UserWarning: No contour levels were found within the data range.

antialiased=True)



Question 7c: Comment on the quality of the decision regions for a bagging classifiers with many estimators when compared to that of only one estimator.

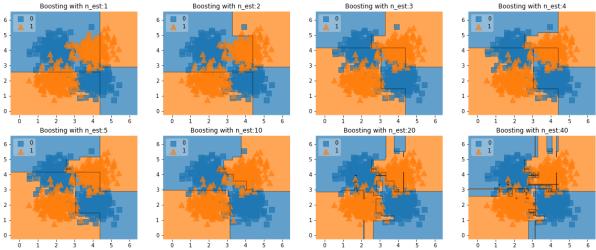
Answer:The quality of the decision region with many estimators (say 10 or 20) is definitely better than the quality of decision region with 1 estimator, implying that model is more refined as the number of sample increases.

Question 7d: **Boosting:** Create boosting classifiers each with n_estimators = 1,2,3,4,5,10, 20, and 40. Use a **Decision Tree** (with max_depth=2) as a base classifier. Using **Data2**, compute the mean **10-fold** cross validation accuracies and standard deviation for each of the bagging classifiers. State your observations on how boosting affected the mean and standard deviation of the base classifier.

```
In [44]:
         dt = DecisionTreeClassifier(max depth=2)
         n est list = [1,2,3,4,5,10,20,40]
         for n est in n est list:
             # create an instance of a boosting classifier with 'n est' estimators
             boosting = AdaBoostClassifier(base estimator=dt, n estimators=n est)
             # compute cross-validation accuracy for each bagging classifier
             scores = cross val score(boosting, Data2 X, Data2 Y, cv=10, scoring='accur
         acy')
             print("Boosting Accuracy: %.2f (+/- %.2f) #estimators: %d" % (scores.mean
         (), scores.std(), n est))
         Boosting Accuracy: 0.88 (+/- 0.03) #estimators: 1
         Boosting Accuracy: 0.88 (+/- 0.03) #estimators: 2
         Boosting Accuracy: 0.90 (+/- 0.04) #estimators: 3
         Boosting Accuracy: 0.90 (+/- 0.04) #estimators: 4
         Boosting Accuracy: 0.92 (+/- 0.03) #estimators: 5
         Boosting Accuracy: 0.92 (+/- 0.04) #estimators: 10
         Boosting Accuracy: 0.91 (+/- 0.04) #estimators: 20
         Boosting Accuracy: 0.91 (+/- 0.02) #estimators: 40
```

^{**}Answer: Boosting accuracy is little low for estimators 1,2,3,4 because it likely underfits the model whereas boosting accuracy for estimators 20 and 40 is little lower because of likely overfitting. Estimators 5 and 10 rightly generalize the decision region to fit the model approximate enough.**

^{**}Question 7e:** Plot decision regions for above boosting classifiers. Explain your reason for what may have lead to the observations in **Question 7d**.



^{**}Answer: From the above plot we can boosting accuracy is little low for estimators 1,2,3,4 because it underfits the model whereas boosting accuracy for estimators 20 and 40 is little lower because of overfitting. Estimators 5 and 10 rightly generalize the decision region.**

8. Classification on a real-world dataset

Real world datasets typically have many attributes making it hard to visualize. This question is about using SVM and Decision Tree algorithms on a real world 'breast cancer' dataset.

The following code reads the dataset from the 'datasets' library in sklearn.

```
In [46]: from sklearn import datasets
   cancer = datasets.load_breast_cancer()
```

The features are:

Class labels are:

```
In [48]: cancer.target_names
Out[48]: array(['malignant', 'benign'], dtype='<U9')</pre>
```

Create dataset for classification

```
In [49]: X = cancer.data
Y = cancer.target
```

Number of samples are:

```
In [50]: X.shape
Out[50]: (569, 30)
```

Question 8a: Of all the SVM classifiers you explored in this hands-on exercise (i.e., linear SVM, SVM with a polynomial kernel and RBF kernel), which SVM results in a highest 10-fold cross-validation accuracy on this dataset? Explore the possible parameters for each SVM to determine the best performance for that SVM. For example, when studying linear SVM, explore a range of C values [0.001, 0.01, 0.1, 1]. Similarly for degree consider [1,2]. For gamma, consider [0.001, 0.01, 0.1, 1, 10, 100].

```
In [51]: #Linear SVM
svm_linear_c_0001 = SVC(C=0.001, kernel='linear')
svm_linear_c_001 = SVC(C=0.01, kernel='linear')
svm_linear_c_01 = SVC(C=0.1, kernel='linear')
svm_linear_c_1 = SVC(C=1, kernel='linear')
```

```
In [52]: svm_linear_scores_c_0001 = cross_val_score(svm_linear_c_0001, X, Y, cv=10, sco
ring='accuracy')
```

```
In [53]: svm_linear_scores_c_001 = cross_val_score(svm_linear_c_001, X, Y, cv=10, scori
ng='accuracy')
```

```
In [54]:
         svm_linear_scores_c_01 = cross_val_score(svm_linear_c_01, X, Y, cv=10, scoring
         ='accuracy')
In [55]:
         svm linear scores c 1 = cross val score(svm linear c 1, X, Y, cv=10, scoring=
          'accuracy')
In [56]:
         svm linear accuracy cancer = pd.DataFrame.from dict({ 'C': ['0.001','0.01','0.
         1','1'],
                                                            'Score': [svm linear scores
         c 0001.mean(),
                                                                      svm linear scores
         c 001.mean(),
                                                                      svm linear scores
         c_01.mean(),
                                                                      svm linear scores
         c 1.mean()]})
         print(svm_linear_accuracy_cancer)
                C
                      Score
            0.001 0.940246
         1
             0.01 0.947236
              0.1 0.947237
         2
                1 0.954318
In [57]: #Polynomial varying C and degree
         #RBF varying C and gamma
         svm poly 1 c 0001 = SVC(C = 0.001, kernel='poly', degree=1, gamma = 'auto')
         svm_poly_1_c_001 = SVC(C = 0.01, kernel='poly', degree=1, gamma = 'auto')
         svm poly 1 c 01 = SVC(C = 0.1, kernel='poly', degree=1, gamma = 'auto')
         svm poly 1 c 1 = SVC(C = 1, kernel='poly', degree=1, gamma = 'auto')
         svm_poly_2_c_0001 = SVC(C = 0.001, kernel='poly', degree=2, gamma = 'auto')
         svm_poly_2_c_001 = SVC(C = 0.01, kernel='poly', degree=2, gamma = 'auto')
         svm_poly_2_c_01 = SVC(C = 0.1, kernel='poly', degree=2, gamma = 'auto')
         svm poly 2 c 1 = SVC(C = 1, kernel='poly', degree=2, gamma = 'auto')
In [58]:
         svm poly scores 1 c 0001 = cross val score(svm poly 1 c 0001, X, Y, cv=10, sco
         ring='accuracy')
         svm poly scores 1 c 001 = cross val score(svm poly 1 c 001, X, Y, cv=10, scori
In [59]:
         ng='accuracy')
In [60]:
         svm_poly_scores_1_c_01 = cross_val_score(svm_poly_1_c_01, X, Y, cv=10, scoring
         ='accuracy')
In [61]:
         svm_poly_scores_1_c_1 = cross_val_score(svm_poly_1_c_1, X, Y, cv=10, scoring=
          'accuracy')
In [62]:
         svm_poly_scores_2_c_0001 = cross_val_score(svm_poly_2_c_0001, X, Y, cv=10, sco
         ring='accuracy')
```

```
In [63]:
         svm poly scores 2 c 001 = cross val score(svm poly 2 c 001, X, Y, cv=10, scori
         ng='accuracy')
         svm poly scores 2 c 01 = cross val score(svm poly 2 c 01, X, Y, cv=10, scoring
In [64]:
         ='accuracy')
In [65]:
         svm poly scores 2 c 1 = cross val score(svm poly 2 c 1, X, Y, cv=10, scoring=
          'accuracy')
In [66]:
         svm poly accuracy cancer = pd.DataFrame.from dict({ 'Degree': ['1','1','1','1'
          ,'2','2','2','2'],
                                                             'C': ['.001','.01','.1','1',
          '.001','.01','.1','1'],
                                                             'Score': [svm poly scores 1
         c_0001.mean(),
                                                                        svm_poly_scores_1_
         c 001.mean(),
                                                                        svm_poly_scores_1_
         c 01.mean(),
                                                                        svm_poly_scores_1_
         c_1.mean(),
                                                                        svm poly scores 2
         c 0001.mean(),
                                                                        svm_poly_scores_2_
         c 001.mean(),
                                                                        svm poly scores 2
         c_01.mean(),
                                                                        svm_poly_scores_2_
         c 1.mean()]})
         print(svm_poly_accuracy_cancer)
           Degree
                             Score
                       C
                1
                    .001
                          0.928027
         1
                1
                          0.940278
                     .01
         2
                1
                      .1
                         0.947267
```

```
3
       1
                0.947267
             1
       2
                0.949085
4
          .001
5
       2
           .01
                0.957920
6
       2
             .1
                 0.957920
       2
                 0.957951
7
             1
```

```
In [67]: #RBF varying C and gamma
         svm rbf 0001 c 0001 = SVC(C = 0.001, kernel = 'rbf', gamma = 0.001)
         svm rbf 0001 c 001 = SVC(C = 0.01, kernel = 'rbf', gamma = 0.001)
         svm rbf 0001 c 01 = SVC(C = 0.1, kernel='rbf', gamma=0.001)
         svm rbf 0001 c 1 = SVC(C = 1, kernel='rbf', gamma=0.001)
         svm rbf 001 c 0001 = SVC(C = 0.001, kernel = 'rbf', gamma = 0.01)
         svm rbf 001 c 001 = SVC(C = 0.01, kernel='rbf', gamma=0.01)
         svm rbf 001 c 01 = SVC(C = 0.1, kernel='rbf', gamma=0.01)
         svm_rbf_001_c_1 = SVC(C = 1, kernel='rbf', gamma=0.01)
         svm_rbf_01_c_0001 = SVC(C = 0.001, kernel='rbf', gamma=0.1)
         svm rbf 01 c 001 = SVC(C = 0.01, kernel='rbf', gamma=0.1)
         svm rbf 01 c 01 = SVC(C = 0.1, kernel='rbf', gamma=0.1)
         svm rbf 01 c 1 = SVC(C = 1, kernel='rbf', gamma=0.1)
         svm rbf 1 c 0001 = SVC(C = 0.001, kernel='rbf', gamma=1)
         svm rbf 1 c 001 = SVC(C = 0.01, kernel='rbf', gamma=1)
         svm_rbf_1_c_01 = SVC(C = 0.1, kernel='rbf', gamma=1)
         svm rbf 1 c 1 = SVC(C = 1, kernel='rbf', gamma=1)
         svm rbf 10 c 0001 = SVC(C = 0.001, kernel='rbf', gamma=10)
         svm rbf 10 c 001 = SVC(C = 0.01, kernel='rbf', gamma=10)
         svm_rbf_10_c_01 = SVC(C = 0.1, kernel='rbf', gamma=10)
         svm rbf 10 c 1 = SVC(C = 1, kernel='rbf', gamma=10)
         svm rbf 100 c 0001 = SVC(C = 0.001, kernel='rbf', gamma=100)
         svm_rbf_100_c_001 = SVC(C = 0.01, kernel='rbf', gamma=100)
         svm rbf 100 c 01 = SVC(C = 0.1, kernel='rbf', gamma=100)
         svm rbf 100 c 1 = SVC(C = 1, kernel='rbf', gamma=100)
```

- In [68]: svm_rbf_scores_0001_c_0001 = cross_val_score(svm_rbf_0001_c_0001, X, Y, cv=10, scoring='accuracy')
- In [70]: svm_rbf_scores_0001_c_01 = cross_val_score(svm_rbf_0001_c_01, X, Y, cv=10, sco ring='accuracy')

- In [73]: svm_rbf_scores_001_c_001 = cross_val_score(svm_rbf_001_c_001, X, Y, cv=10, sco ring='accuracy')

- In [75]: svm_rbf_scores_001_c_1 = cross_val_score(svm_rbf_001_c_1, X, Y, cv=10, scoring = 'accuracy')
- In [76]: svm_rbf_scores_01_c_0001 = cross_val_score(svm_rbf_01_c_0001, X, Y, cv=10, sco ring='accuracy')
- In [77]: svm_rbf_scores_01_c_001 = cross_val_score(svm_rbf_01_c_001, X, Y, cv=10, scori
 ng='accuracy')

- In [84]: svm_rbf_scores_10_c_0001 = cross_val_score(svm_rbf_10_c_0001, X, Y, cv=10, scoring='accuracy')
- In [85]: svm_rbf_scores_10_c_001 = cross_val_score(svm_rbf_10_c_001, X, Y, cv=10, scori
 ng='accuracy')
- In [87]: svm_rbf_scores_10_c_1 = cross_val_score(svm_rbf_10_c_1, X, Y, cv=10, scoring=
 'accuracy')
- In [88]: svm_rbf_scores_100_c_0001 = cross_val_score(svm_rbf_100_c_0001, X, Y, cv=10, s
 coring='accuracy')
- In [90]: svm_rbf_scores_100_c_01 = cross_val_score(svm_rbf_100_c_01, X, Y, cv=10, scori
 ng='accuracy')

In [91]: svm_rbf_scores_100_c_1 = cross_val_score(svm_rbf_100_c_1, X, Y, cv=10, scoring = 'accuracy')

```
In [92]:
         svm rbf accuracy cancer = pd.DataFrame.from dict({ 'Gamma': ['.001','.001','.0
          01','.001',
                                                                          '.01','.01','.01'
          ,'.01',
                                                                          '.1','.1','.1','.
         1',
                                                                          '1','1','1','1',
                                                                          '10','10','10','1
          0',
                                                                          '100','100','100'
          ,'100'],
                                                              'C': ['.001','.01','.1','1',
                                                                     '.001','.01','.1','1',
                                                                     '.001','.01','.1','1',
                                                                     '.001','.01','.1','1',
                                                                     '.001','.01','.1','1',
                                                                     '.001','.01','.1','1'
          ],
                                                              'Score': [
                                                                         svm rbf scores 000
          1 c 0001.mean(),
                                                                         svm_rbf_scores_000
          1 c 001.mean(),
                                                                         svm_rbf_scores_000
          1 c 01.mean(),
                                                                         svm rbf scores 000
          1 c 1.mean(),
                                                                         svm_rbf_scores_000
          1 c 0001.mean(),
                                                                         svm_rbf_scores_001
          _c_001.mean(),
                                                                         svm_rbf_scores_001
          _c_01.mean(),
                                                                         svm_rbf_scores_001
          _c_1.mean(),
                                                                         svm rbf scores 01
          c 0001.mean(),
                                                                         svm_rbf_scores_01_
         c 001.mean(),
                                                                         svm_rbf_scores_01_
          c_01.mean(),
                                                                         svm_rbf_scores_01_
          c_1.mean(),
                                                                         svm_rbf_scores_1_c
          0001.mean(),
                                                                         svm_rbf_scores_1_c
          _001.mean(),
                                                                         svm_rbf_scores_1_c
          01.mean(),
                                                                         svm_rbf_scores_1_c
          1.mean(),
                                                                         svm_rbf_scores_10_
          c_0001.mean(),
                                                                         svm_rbf_scores_10_
          c_001.mean(),
                                                                         svm_rbf_scores_10_
```

```
C
   Gamma
                    Score
0
    .001
                0.627427
          .001
1
    .001
           .01
                0.627427
2
    .001
                0.627427
            . 1
3
    .001
             1 0.924242
4
     .01
          .001 0.627427
5
     .01
           .01
                0.627427
     .01
            .1
                0.627427
7
     .01
             1 0.632660
8
          .001 0.627427
      .1
9
      .1
           .01 0.627427
      .1
10
                0.627427
            .1
11
      .1
             1 0.627427
12
       1
          .001
                0.627427
13
       1
           .01 0.627427
            .1 0.627427
14
       1
15
       1
             1
                0.627427
16
      10
          .001 0.627427
17
      10
           .01
                0.627427
18
      10
            .1 0.627427
19
      10
             1 0.627427
20
     100
          .001 0.627427
21
     100
           .01 0.627427
22
     100
            .1 0.627427
23
     100
             1 0.627427
```

Question 8b: Similar to **Question 8a** explore decision trees with different max_depth to determine which values returns the best classifier.

```
In [93]: dt2_score_cancer = cross_val_score(dt2, X, Y, cv=10, scoring='accuracy')
In [94]: dt4_score_cancer = cross_val_score(dt4, X, Y, cv=10, scoring='accuracy')
In [95]: dt6_score_cancer = cross_val_score(dt6, X, Y, cv=10, scoring='accuracy')
```

^{**}Answer: SVM Polynomial with degree 2 has the best accuracy with .977951. Generally SVM Polynomial classifier seems to be performing better on this data with SVM Linear a close second. SVM RBF performance appears to be very substandard**

```
In [96]: dt8 score cancer = cross val score(dt8, X, Y, cv=10, scoring='accuracy')
 In [97]:
          dt10 score cancer = cross val score(dt10, X, Y, cv=10, scoring='accuracy')
 In [98]:
          dt50 score cancer = cross val score(dt50, X, Y, cv=10, scoring='accuracy')
In [100]:
          dt_accuracy_cancer = { 'Depth': [2,4,6,8,10,50],
               'Score': [dt2 score cancer.mean(),dt4 score cancer.mean(),dt6 score cancer
           .mean(),dt8 score cancer.mean(),
                        dt10_score_cancer.mean(), dt50_score.mean()]
          dt accuracy df cancer = pd.DataFrame.from dict(dt accuracy cancer)
          print(dt_accuracy_df_cancer)
             Depth
                       Score
          0
                 2
                    0.919378
          1
                 4 0.922858
          2
                 6 0.919442
          3
                 8 0.912330
          4
                10 0.917656
          5
                50 0.945000
```

Question 8c: Imagine a scenario where you are working at a cancer center as a data scientist tasked with identifying the characteristics that distinguish malignant tumors from benign tumors. Based on your knowledge of classification techniques which approach would you use and why?

```
In [104]: cancer.data
Out[104]: 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-021,
                  [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,
                  7.039e-02]])
          cancer_df = pd.DataFrame(data=cancer.data, columns=cancer.feature_names)
In [106]:
```

^{**}Answer: DT with MaxDepth = 50 is the best performer on the data**

In [111]: cancer_df.info()

<class 'pandas.core.frame.DataFrame'> RangeIndex: 569 entries, 0 to 568 Data columns (total 30 columns): mean radius 569 non-null float64 569 non-null float64 mean texture mean perimeter 569 non-null float64 569 non-null float64 mean area mean smoothness 569 non-null float64 569 non-null float64 mean compactness 569 non-null float64 mean concavity 569 non-null float64 mean concave points mean symmetry 569 non-null float64 mean fractal dimension 569 non-null float64 radius error 569 non-null float64 569 non-null float64 texture error 569 non-null float64 perimeter error 569 non-null float64 area error smoothness error 569 non-null float64 compactness error 569 non-null float64 concavity error 569 non-null float64 concave points error 569 non-null float64 symmetry error 569 non-null float64 fractal dimension error 569 non-null float64 worst radius 569 non-null float64 worst texture 569 non-null float64 569 non-null float64 worst perimeter 569 non-null float64 worst area worst smoothness 569 non-null float64 worst compactness 569 non-null float64 worst concavity 569 non-null float64 worst concave points 569 non-null float64 worst symmetry 569 non-null float64 worst fractal dimension 569 non-null float64 dtypes: float64(30) memory usage: 133.5 KB

In [108]: cancer_df.corr()

Out[108]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	со
mean radius	1.000000	0.323782	0.997855	0.987357	0.170581	0.506124	0.6
mean texture	0.323782	1.000000	0.329533	0.321086	-0.023389	0.236702	0.3
mean perimeter	0.997855	0.329533	1.000000	0.986507	0.207278	0.556936	0.7
mean area	0.987357	0.321086	0.986507	1.000000	0.177028	0.498502	0.6
mean smoothness	0.170581	-0.023389	0.207278	0.177028	1.000000	0.659123	0.5
mean compactness	0.506124	0.236702	0.556936	0.498502	0.659123	1.000000	8.0
mean concavity	0.676764	0.302418	0.716136	0.685983	0.521984	0.883121	1.0
mean concave points	0.822529	0.293464	0.850977	0.823269	0.553695	0.831135	0.9
mean symmetry	0.147741	0.071401	0.183027	0.151293	0.557775	0.602641	0.5
mean fractal dimension	-0.311631	-0.076437	-0.261477	-0.283110	0.584792	0.565369	0.3
radius error	0.679090	0.275869	0.691765	0.732562	0.301467	0.497473	0.6
texture error	-0.097317	0.386358	-0.086761	-0.066280	0.068406	0.046205	0.0
perimeter error	0.674172	0.281673	0.693135	0.726628	0.296092	0.548905	0.6
area error	0.735864	0.259845	0.744983	0.800086	0.246552	0.455653	0.6
smoothness error	-0.222600	0.006614	-0.202694	-0.166777	0.332375	0.135299	0.0
compactness error	0.206000	0.191975	0.250744	0.212583	0.318943	0.738722	0.6
concavity error	0.194204	0.143293	0.228082	0.207660	0.248396	0.570517	0.6
concave points error	0.376169	0.163851	0.407217	0.372320	0.380676	0.642262	0.6
symmetry error	-0.104321	0.009127	-0.081629	-0.072497	0.200774	0.229977	0.1

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	со
fractal dimension error	-0.042641	0.054458	-0.005523	-0.019887	0.283607	0.507318	0.4
worst radius	0.969539	0.352573	0.969476	0.962746	0.213120	0.535315	0.6
worst texture	0.297008	0.912045	0.303038	0.287489	0.036072	0.248133	0.2
worst perimeter	0.965137	0.358040	0.970387	0.959120	0.238853	0.590210	0.7
worst area	0.941082	0.343546	0.941550	0.959213	0.206718	0.509604	0.6
worst smoothness	0.119616	0.077503	0.150549	0.123523	0.805324	0.565541	0.4
worst compactness	0.413463	0.277830	0.455774	0.390410	0.472468	0.865809	0.7
worst concavity	0.526911	0.301025	0.563879	0.512606	0.434926	0.816275	8.0
worst concave points	0.744214	0.295316	0.771241	0.722017	0.503053	0.815573	8.0
worst symmetry	0.163953	0.105008	0.189115	0.143570	0.394309	0.510223	0.4
worst fractal dimension	0.007066	0.119205	0.051019	0.003738	0.499316	0.687382	0.5

30 rows × 30 columns

In [112]: from sklearn.feature_selection import SelectKBest from sklearn.feature_selection import chi2

```
In [113]: #apply SelectKBest class to extract top 10 best features
bestfeatures = SelectKBest(score_func=chi2, k=10)
fit = bestfeatures.fit(X,Y)
dfscores = pd.DataFrame(fit.scores_)
dfcolumns = pd.DataFrame(cancer.feature_names)
#concat two dataframes for better visualization
featureScores = pd.concat([dfcolumns,dfscores],axis=1)
featureScores.columns = ['Specs','Score'] #naming the dataframe columns
print(featureScores.nlargest(10,'Score')) #print 10 best features
```

	Specs	Score
23	worst area	112598.431564
3	mean area	53991.655924
13	area error	8758.504705
22	worst perimeter	3665.035416
2	mean perimeter	2011.102864
20	worst radius	491.689157
0	mean radius	266.104917
12	perimeter error	250.571896
21	worst texture	174.449400
1	mean texture	93.897508

**Answer:

I can use the above technique i.e. univariate selection find out the top 10 features which influence the prediction. source(https://towardsdatascience.com/feature-selection-techniques-in-machine-learning-with-python-f24e7da3f36e)

For classification I would use SVM Poly of Deg 2 with C = 1 since it has the best accuracy rate although the execution is very slow, as it would reduce the attribution of Cancer, which again if wrongly attributed would cause immense trauma to the patient either ways

**