

22         False         Fa		False	False	False	False	False	False	False
Pale	21	False	False	False	False	False	False	False
Pale	22	False	False	False	False	False	False	False
False								
Pale	23	False	False	False	False	False	False	True
False	24	False	False	False	False	False	False	False
False	25	False	False	False	False	False	False	False
False	26	False	False	False	False	False	False	False
False								
False								
False	28	False	False	False	False	False	False	False
Falce	29	False	False	False	False	False	False	False
Falce								
Faire		Falso	False	Falso	Falsa	Falco	Falsa	Falce
### False   Fa								
Fabre	670	False	False	False	False	False	False	False
### Fabre   Fa	671	False	False	False	False	False	False	False
Fabre	672	False	False	False	False	False	False	False
Fabre	673	False	False	False	False	False	False	False
### False   Fa								
### False   Fa								
False	675	False	False	False	False	False	False	False
False	676	False	False	False	False	False	False	False
False	677	False	False	False	False	False	False	False
False								
False								
False	679	False	False	False	False	False	False	False
	680	False	False	False	False	False	False	False
	681	False	False	False	False	False	False	False
683								
False								
False	683	False	False	False	False	False	False	False
False	684	False	False	False	False	False	False	False
False	685	False	False	False	False	False	False	False
False	686	Falso	False	False	Falsa	False	Falsa	Fale
False								
False	687	False	False	False	False	False	False	Fals
False   Fals	688	False	False	False	False	False	False	Fals
False   Fals	689	False	False	False	False	False	False	Fals
False   Fals	690	False	False	False	False	False	False	Fals
False								
False								
### False   Fa	692	False	False	False	False	False	False	Fals
False	693	False	False	False	False	False	False	False
False	694	False	False	False	False	False	False	Fals
False								
## False   Fal								
False   Fals	696	False	False	False	False	False	False	Fals
dataset.isnull().sum()  Sample_code_number	697	False	False	False	False	False	False	Fals
dataset.isnull().sum()  Sample.code_number	698	False	False	False	False	False	False	Fals
dataset.isnull().sum()  Sample_code_number								
dataset.isnull().sum()  Sample_code_number	699 rows x 11 column	18						
Sample_code_number	4							
Sample_code_number								
Clump_Thickness 0 Uniformity_of_Cell_Size 0 Uniformity_of_Cell_Shape 0 Marginal_Adhesion 0 Single_Epithelial_Cell_Size 0 Bare_Nuclei 16 Bland_Chromatin 0 Normal_Nucleoli 0 Mitoses 0 dtype: int64  dataset.dropna(inplace=True)  dataset.isnull().sum()  Sample_code_number 0 Clump_Thickness 0 Uniformity_of_Cell_Size 0 Uniformity_of_Cell_Size 0 Uniformity_of_Cell_Size 0 Uniformity_of_Cell_Size 0 Uniformity_of_Cell_Size 0 Single_Epithelial_Cell_Size 0 Bare_Nuclei 0 Bland_Chromatin 0 Normal_Nucleoli 0 Normal_Nucleoli 0 Normal_Nucleoli 0 Normal_Nucleoli 0 Mitoses 0 dtype: int64  dataset.drop("Sample_code_number", axis=1, inplace=True)		sum()						
Uniformity_of_Cell_Slape 0 Wniformity_of_Cell_Shape 0 Mangdinal_Adhesion 0 Single_Epithelial_Cell_Size 0 Bare_Nuclei 16 Bland_chromatin 0 Normal_Nucleoli 0 Mitoses 0 Class 0 dtype: int64  dataset.dropna(inplace=True)  dataset.isnull().sum()  Sample_code_number 0 Clump_Thickness 0 Uniformity_of_Cell_Slape 0 Uniformity_of_Cell_Shape 0 Mangdinal_Adhesion 0 Single_Epithelial_Cell_Size 0 Bland_chromatin 0 Normal_Nucleoli 0 Bland_chromatin 0 Normal_Nucleoli 0 Bland_chromatin 0 Normal_Nucleoli 0 Mormal_Nucleoli 0 Mormal_Mormal_Nucleoli 0 Mormal_Mormal_Nucleoli 0 Mormal_Mormal_Mormal_Mormal_Mormal_Mormal_Mormal_Mormal_Mormal_Mormal_Mormal_Mor	<pre>dataset.isnull().</pre>							
Uniformity_of_Cell_Shape 0 Marginal_Adhesion 0 Single_Epithelial_Cell_Size 0 Bare_Nuclei 16 Bland_Chromatin 0 Normal_Nucleoli 0 Mitoses 0 dtype: int64  dataset.dropna(inplace=True)  dataset.isnull().sum()  Sample_code_number 0 Clump_Thickness 0 Uniformity_of_Cell_Size 0 Uniformity_of_Cell_Shape 0 Marginal_Adhesion 0 Single_Epithelial_Cell_Size 0 Bare_Nuclei 0 Bland_Chromatin 0 Normal_Nucleoli 0 Normal_Nucleoli 0 Normal_Nucleoli 0 Normal_Nucleoli 0 Normal_Nucleoli 0 Mitoses 0 dtype: int64  dataset.drop("Sample_code_number", axis=1, inplace=True)		r	0					
Manginal_Adhesion         0           Single_Epithelial_Cell_Size         0           Bland_Chromatin         0           Normal_Nucleoli         0           Mitoses         0           Class         0           dtype: int64    dataset.dropna(inplace=True)  dataset.dropna(inplace=True)  dataset.isnull().sum()  Sample_code_number         0           Clump_Thickness         0           Uniformity_of_Cell_Size         0           Uniformity_of_Cell_Size         0           Uniformity_of_Cell_Shape         0           Marginal_Adhesion         0           Single_Epithelial_Cell_Size         0           Bane_Nuclei         0           Bland_Chromatin         0           Normal_Nucleoli         0           Mitoses         0           Class         0           dtype: int64         dataset.drop("Sample_code_number", axis=1, inplace=True)	Sample_code_number		0					
Single_Epithelial_Cell_Size	Sample_code_number Clump_Thickness Uniformity_of_Cel	l_Size	0 0					
Bland_Chromatin	Sample_code_number Clump_Thickness Uniformity_of_Cel Uniformity_of_Cel	l_Size l_Shape	9 9 9					
Normal_Nucleoli	Sample_code_number Clump_Thickness Uniformity_of_Cel Uniformity_of_Cel Marginal_Adhesion	l_Size l_Shape	0 0 0 0					
Mitoses 0 Class 0 dtype: int64   dataset.dropna(inplace=True)   dataset.isnull().sum()  Sample_code_number 0 Clump_Thickness 0 Uniformity_of_Cell_Size 0 Uniformity_of_Cell_Shape 0 Marginal_Adhesion 0 Single_Epithelial_Cell_Size 0 Bare_Nuclei 0 Bland_Chromatin 0 Normal_Nucleoli 0 Mitoses 0 Class 0 dtype: int64   dataset.drop("Sample_code_number", axis=1, inplace=True)	Sample_code_number Clump_Thickness Uniformity_of_Cel Uniformity_of_Cel Marginal_Adhesion Single_Epithelial Bare_Nuclei	l_Size l_Shape	0 0 0 0 0 16					
Class dtype: int64  dataset.dropna(inplace=True)  dataset.isnull().sum()  Sample_code_number	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin	l_Size l_Shape	0 0 0 0 16 0					
dataset.dropna(inplace=True)  dataset.isnull().sum()  Sample_code_number	Sample_code_number Clump_Thickness Uniformity_of_cel Uniformity_of_cel Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli	l_Size l_Shape	0 0 0 0 0 16 0					
dataset.isnull().sum()  Sample_code_number	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses	l_Size l_Shape	0 0 0 0 0 16 0 0					
dataset.isnull().sum()  Sample_code_number	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class	l_Size l_Shape	0 0 0 0 0 16 0 0					
Sample_code_number	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class	l_Size l_Shape	0 0 0 0 0 16 0 0					
Clump_Thickness	Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64	l_Size l_Shape _Cell_Size	0 0 0 0 0 16 0 0 0					
Clump_Thickness	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal Nucleoli Mitoses Class dtype: int64	l_Size l_Shape _Cell_Size place=True)	0 0 0 0 0 16 0 0 0					
Uniformity_of_Cell_Shape	Sample_code_number Clump_Thickness Uniformity_of_cel Uniformity_of_cel Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64 dataset.dropna(in	l_Size l_Shape _Cell_Size place=True)	0 0 0 0 0 16 0 0 0					
Marginal_Adhesion 0 Single_Epithelial_Cell_Size 0 Bare_Nuclei 0 Bland_Chromatin 0 Normal_Nucleoli 0 Mitoses 0 Class 0 dtype: int64  dataset.drop("Sample_code_number", axis=1, inplace=True)	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal Nucleoli Mitoses Class dtype: int64  dataset.dropna(in) dataset.isnull(). Sample_code_number	l_Size l_Shape _Cell_Size place=True)	0 0 0 0 16 0 0 0					
Single_Epithelial_Cell_Size	Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in  dataset.isnull(). Sample_code_number Clump_Thickness Uniformity_of_cel:	l_Size l_Shape _Cell_Size  place=True)  sum() r l_Size	0 0 0 0 0 16 0 0 0 0					
Bare_Nuclei	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in) dataset.isnull(). Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel:	l_Size l_Shape _Cell_Size  place=True)  sum() r l_Size l_Shape	0 0 0 0 16 0 0 0					
Bland_Chromatin 0 Normal_Nucleoli 0 Mitoses 0 Class 0 dtype: int64  dataset.drop("Sample_code_number", axis=1, inplace=True)	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in  dataset.isnull(). Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion	l_Size l_Shape _Cell_Size  place=True)  sum()  r  l_Size l_Shape	0 0 0 0 16 0 0 0 0					
Mitoses 0 Class 0 dtype: int64  dataset.drop("Sample_code_number", axis=1, inplace=True)	Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in  dataset.isnull().  Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial	l_Size l_Shape _Cell_Size  place=True)  sum()  r  l_Size l_Shape	0 0 0 0 0 0 0 0 0 0 0 0					
Class 0 dtype: int64  dataset.drop("Sample_code_number", axis=1, inplace=True)	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal Nucleoli Mitoses Class dtype: int64  dataset.dropna(in)  dataset.isnull().  Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin	l_Size l_Shape _Cell_Size  place=True)  sum()  r  l_Size l_Shape	0 0 0 0 16 0 0 0 0					
<pre>dtype: int64  dataset.drop("Sample_code_number", axis=1, inplace=True)</pre>	Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in  dataset.isnull().  Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Bare_Nuclei Bland_Chromatin Normal_Nucleoli	l_Size l_Shape _Cell_Size  place=True)  sum()  r  l_Size l_Shape	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0					
dataset.drop("Sample_code_number", axis=1, inplace=True)	Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in  dataset.isnull().  Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses	l_Size l_Shape _Cell_Size  place=True)  sum()  r  l_Size l_Shape	0 0 0 0 0 16 0 0 0 0 0 0 0 0 0 0 0 0 0 0					
	Sample_code_number Clump_Thickness Uniformity_of_Cel: Uniformity_of_Cel: Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal Nucleoli Mitoses Class dtype: int64  dataset.dropna(in)  dataset.isnull(). Sample_code_number Clump_Thickness Uniformity_of_Cel: Marginal_Adhesion Single_Epithelial_ Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class	l_Size l_Shape _Cell_Size  place=True)  sum()  r  l_Size l_Shape	0 0 0 0 0 16 0 0 0 0 0 0 0 0 0 0 0 0 0 0					
dataset.head(5)	Sample_code_number Clump_Thickness Uniformity_of_Cel! Uniformity_of_Cel! Uniformity_of_Cel! Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in) dataset.isnull(). Sample_code_number Clump_Thickness Uniformity_of_Cel! Uniformity_of_Cel! Uniformity_of_Cel! Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class	l_Size l_Shape _Cell_Size  place=True)  sum()  r  l_Size l_Shape	0 0 0 0 0 16 0 0 0 0 0 0 0 0 0 0 0 0 0 0					
	Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Marginal_Adhesion Single_Epithelial Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64  dataset.dropna(in  dataset.isnull().  Sample_code_number Clump_Thickness Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Uniformity_of_cel: Bare_Nuclei Bland_Chromatin Normal_Nucleoli Mitoses Class dtype: int64	l_Size l_Shape _Cell_Size  place=True)  sum()  r l_Size l_Shape _Cell_Size	0 0 0 0 0 16 0 0 0 0 0	place=True)				

```
0
                                                                                                                         2
                              6
                                                                             8
                                                                                                                                    4.0
             3
                              4
                                                                                                3
                                                                                                                         2
                                                                                                                                    1.0
                                                                                                                                                      3
            4
In [226]: X = dataset.drop("Class", axis=1)
           y = dataset["Class"]
In [227]: X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=4)
In [228]: modelLRC = LogisticRegression()
modelSVMC = svm.SVC(kernel='linear')
modelKNNC = KNeighborsClassifier(n_neighbors=3)
In [229]: modelLRC.fit(X_train, y_train)
Out[229]: LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True, intercept_scaling=1, max_iter=100, multi_class='ovr', n_jobs=1, penalty='l2', random_state=None, solver='liblinear', tol=0.0001,
                       verbose=0, warm_start=False)
In [230]: modelSVMC.fit(X_train, y_train)
Out[230]: SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
              decision_function_shape='ovr', degree=3, gamma='auto', kernel='linear',
max_iter=-1, probability=False, random_state=None, shrinking=True,
              tol=0.001, verbose=False)
In [231]: modelKNNC.fit(X_train, y_train)
Out[231]: KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                        metric_params=None, n_jobs=1, n_neighbors=3, p=2,
                         weights='uniform')
In [232]: predictionLRC = modelLRC.predict(X_test)
    predictionSVMC = modelSVMC.predict(X_test)
    predictionKNNC = modelKNNC.predict(X_test)
In [233]: print("Confusion Matrix for Logistic Regression: ")
            confusion_matrix(y_test,predictionLRC)
              Confusion Matrix for Logistic Regression:
Out[233]: array([[125, 7], [ 3, 70]], dtype=int64)
In [234]: print("Confusion Matrix for Support Vector Machine: ")
            confusion_matrix(y_test,predictionSVMC)
              Confusion Matrix for Support Vector Machine:
Out[234]: array([[122, 10],
                    [ 3, 70], dtype=int64)
In [235]: print("Confusion Matrix for KNN where (N=3): ")
            confusion_matrix(y_test,predictionKNNC)
              Confusion Matrix for KNN where (N=3):
Out[235]: array([[126, 6], [ 2, 71]], dtype=int64)
In [236]: LR = accuracy_score(y_test,predictionLRC)*100
            SVM = accuracy_score(y_test,predictionSVMC)*100
KNN = accuracy_score(y_test,predictionKNNC)*100
In [237]: #SVM = accuracy_score(y_test,predictionSVMC)*100
In [238]: #KNN = accuracy_score(y_test, predictionKNNC)*100
In [239]: print("Accuracy Chart: ")
            print("Logistic Regression: ",LR)
            print("Support Vector Machine: ",SVM)
            print("K-Nearest Neighbors (where k=3): ",KNN)
            #sorted([LR, SVM, KNN], reverse=True)
              Accuracy Chart:
              Logistic Regression: 95.1219512195122
              Support Vector Machine: 93.65853658536587
              K-Nearest Neighbors (where k=3): 96.09756097560975
In [240]: if((LR>SVM) and (LR>KNN)) :
                 print("Logistic Regression has highest accuracy: ", LR)
                 if(SVM>KNN):
                     print("Support Vectro Machine stands in the middle: ", SVM)
                     print("K-Nearest Neighbor has least accuracy: ", KNN)
                     print("K-Nearest Neighbor stands in the middle: ", KNN)
                     print("Support Vectro Machine has least accuracy: ", SVM)
            elif((SVM>LR) and (SVM>KNN)):
                 print("Support Vectro Machine has highest accuracy: ", SVM)
                 if(LR>KNN):
                     print("Logistic Regression stands in the middle: "
                     print("K-Nearest Neighbor has least accuracy: ", KNN)
                 else:
```

```
print("Logistic Regression has least accuracy: ", LR)

else:
    print("K-Nearest Neighbor has highest accuracy: ", KNN)
    if(LR>SVM):
        print("Logistic Regression stands in the middle: ", LR)
        print("Support Vectro Machine has least accuracy: ", SVM)
    else:
        print("Support Vectro Machine stands in the middle: ", SVM)
        print("Logistic Regression has least accuracy: ", LR)

K-Nearest Neighbor has highest accuracy: 96.09756097560975
    Logistic Regression stands in the middle: 95.1219512195122
    Support Vectro Machine has least accuracy: 93.65853658536587
```