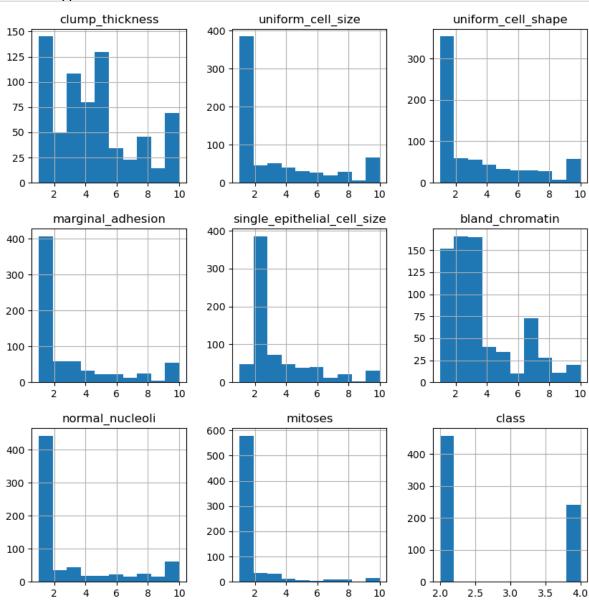
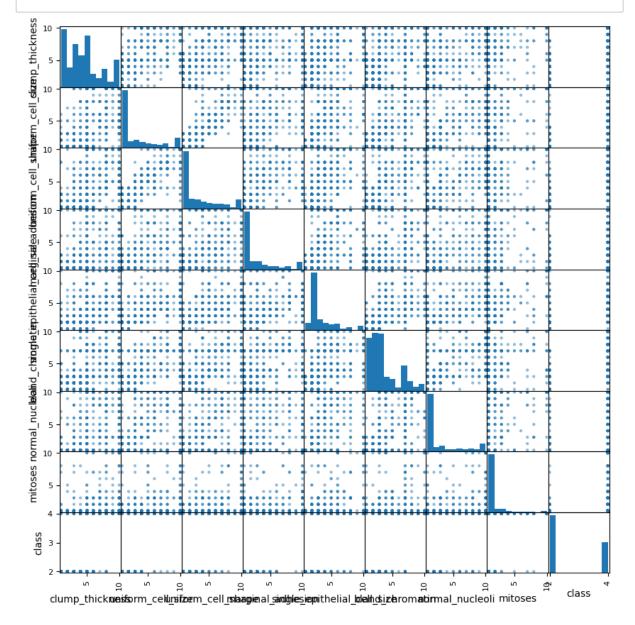
```
In [80]:
         import numpy as np
          from sklearn import preprocessing
          from sklearn.neighbors import KNeighborsClassifier
          from sklearn.svm import SVC
          from sklearn.model selection import train test split
          from sklearn import model selection
          from sklearn.metrics import classification report, accuracy score
          from pandas.plotting import scatter matrix
          import matplotlib.pyplot as plt
          import pandas as pd
In [81]: # Loading the Dataset
          #http://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wiscon
          url = "https://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer
          names = ['id','clump_thickness','uniform_cell_size','uniform_cell_shape','marg
          #data frame
          df = pd.read_csv(url, names=names)
                                                                                           \blacktriangleright
In [82]: print(df.describe())
                                clump_thickness
                                                 uniform_cell_size uniform_cell_shape
          \
          count
                 6.990000e+02
                                     699.000000
                                                         699.000000
                                                                              699.000000
                 1.071704e+06
                                       4.417740
                                                           3.134478
                                                                                3.207439
          mean
          std
                 6.170957e+05
                                       2.815741
                                                           3.051459
                                                                                2.971913
          min
                 6.163400e+04
                                       1.000000
                                                           1.000000
                                                                                1.000000
          25%
                 8.706885e+05
                                       2.000000
                                                           1.000000
                                                                                1.000000
          50%
                 1.171710e+06
                                       4.000000
                                                           1.000000
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          75%
                 1.238298e+06
                                       6.000000
                                                           5.000000
                                                                                5.000000
                 1.345435e+07
                                      10.000000
                                                          10.000000
                                                                               10.000000
          max
                                     single_epithelial_cell_size
                                                                    bland chromatin
                 marginal adhesion
          count
                        699.000000
                                                       699.000000
                                                                         699.000000
          mean
                          2.806867
                                                         3.216023
                                                                           3.437768
          std
                          2.855379
                                                         2.214300
                                                                           2.438364
          min
                          1.000000
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          25%
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                 normal nucleoli
                                      mitoses
                                                     class
          count
                      699.000000
                                   699.000000
                                               699.000000
          mean
                        2.866953
                                     1.589413
                                                  2.689557
          std
                        3.053634
                                     1.715078
                                                  0.951273
          min
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                                     1.000000
                                                  4.000000
                       10.000000
                                    10.000000
                                                  4.000000
          max
```

```
In [83]: # Preprocess the data
         # ? =missing values in dataset; -9999 means ignore them
         df.replace('?',-9999,inplace=True)
         print(df.axes)
         #class= 4=>malignant(cancerous) ,2=>benign
         #drop 'id' column because it does not contributes to dataset and may result in
         df.drop(['id'],1,inplace=True)
         #shape of dataset
         print(df.shape)
         [RangeIndex(start=0, stop=699, step=1), Index(['id', 'clump_thickness', 'unif
         orm_cell_size', 'uniform_cell_shape',
                'marginal_adhesion', 'single_epithelial_cell_size', 'bare_nuclei',
                 'bland_chromatin', 'normal_nucleoli', 'mitoses', 'class'],
               dtype='object')]
         (699, 10)
         C:\Users\Sayan\AppData\Local\Temp\ipykernel_5440\2424456935.py:8: FutureWarni
         ng: In a future version of pandas all arguments of DataFrame.drop except for
         the argument 'labels' will be keyword-only.
           df.drop(['id'],1,inplace=True)
```

```
uniform_cell_size
       clump_thickness
                                             uniform cell shape
            699.000000
                                 699.000000
                                                      699.000000
count
               4.417740
                                   3.134478
                                                        3.207439
mean
std
               2.815741
                                   3.051459
                                                        2.971913
               1.000000
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min
25%
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                                                        1.000000
50%
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                                   1.000000
                                                        1.000000
75%
               6.000000
                                   5.000000
                                                        5.000000
max
              10.000000
                                  10.000000
                                                       10.000000
       marginal_adhesion
                           single_epithelial_cell_size
                                                          bland_chromatin
               699.000000
                                              699.000000
                                                                699.000000
count
                 2.806867
                                                3.216023
                                                                  3.437768
mean
std
                 2.855379
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min
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max
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       normal nucleoli
                            mitoses
                                           class
count
            699.000000
                         699.000000
                                      699.000000
               2.866953
                           1.589413
                                        2.689557
mean
std
               3.053634
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min
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                                        2.000000
75%
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                           1.000000
                                        4.000000
max
              10.000000
                          10.000000
                                        4.000000
```

In [85]: #Plot histograms for each feature to understand distribution
 df.hist(figsize=(10,10))
 plt.show()





```
In [87]:
         #create X and Y datasets for training
         print(df.loc[0])
         X = np.array(df.drop(['class'],1))
         print('class deleted')
         print(X[0])
         y = np.array(df['class'])
         print(y[0])
         print(X.shape,y.shape)
         # No_of_rows X no_of_columns
         #(no_of_rows,) => n X 1 vector or n-dim vector
         X_train, X_test, y_train, y_test = model_selection.train_test_split(X,y,test_s
         print(X_train.shape, y_train.shape)
         print(X test.shape, y test.shape)
                                         5
         clump thickness
         uniform cell size
                                         1
         uniform_cell_shape
                                         1
         marginal adhesion
                                         1
         single_epithelial_cell_size
                                         2
         bare_nuclei
                                         1
                                         3
         bland chromatin
                                         1
         normal nucleoli
                                         1
         mitoses
         class
                                         2
         Name: 0, dtype: object
         class deleted
         [5 1 1 1 2 '1' 3 1 1]
         (699, 9) (699,)
         (559, 9) (559,)
         (140, 9) (140,)
         C:\Users\Sayan\AppData\Local\Temp\ipykernel 5440\2810470274.py:3: FutureWarni
         ng: In a future version of pandas all arguments of DataFrame.drop except for
         the argument 'labels' will be keyword-only.
           X = np.array(df.drop(['class'],1))
In [88]: #specify testing parameters
         seed = 8 #not a random seed for reproducable results
         scoring = 'accuracy'
```

```
In [93]: #define the models to train
         models = []
         models.append(('KNN',KNeighborsClassifier(n_neighbors=5)))# odd value to avoid
         models.append(('SVM',SVC()))
         #Evaluate each model
         results = []
         names = []
         for name, model in models:
             kfold = model_selection.KFold(n_splits=10, random_state=seed, shuffle=True
             cv_results =model_selection.cross_val_score(model,X_train,y_train,cv=kfold
             results.append(cv_results)
             names.append(name)
             msg="%s: %f (%f)" % (name,cv_results.mean(),cv_results.std())
             print(msg) #accuracy only on training data
         print(results)
         4
         KNN: 0.962403 (0.016942)
         SVM: 0.652922 (0.070746)
         [array([0.98214286, 0.96428571, 0.94642857, 0.96428571, 1.
```

([0.64285714, 0.53571429, 0.76785714, 0.69642857, 0.75

0.94642857, 0.96428571, 0.94642857, 0.96428571, 0.94545455]), array

0.64285714, 0.55357143, 0.625 , 0.67857143, 0.63636364])]

## In [94]: #Make predictions on validation dataset for name, model in models: model.fit(X\_train, y\_train) #training the model predictions = model.predict(X\_test) print(name) print(accuracy\_score(y\_test, predictions))

## KNN

## 0.9714285714285714

0.07112007112	037 = 1			
	precision	recall	f1-score	support
2	0.98	0.98	0.98	93
4	0.96	0.96	0.96	47
accuracy			0.97	140
macro avg	0.97	0.97	0.97	140
weighted avg	0.97	0.97	0.97	140
SVM				
0.66428571428	57143			
	precision	recall	f1-score	support
2	0.66	1.00	0.80	93
4	0.00	0.00	0.00	47
accuracy			0.66	140
macro avg	0.33	0.50	0.40	140
weighted avg	0.44	0.66	0.53	140

print(classification report(y test,predictions))

C:\Users\Sayan\anaconda3\lib\site-packages\sklearn\metrics\\_classification.p y:1344: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero\_division` parameter to control this behavior.

\_warn\_prf(average, modifier, msg\_start, len(result))

C:\Users\Sayan\anaconda3\lib\site-packages\sklearn\metrics\\_classification.p y:1344: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero\_division` parameter to control this behavior.

\_warn\_prf(average, modifier, msg\_start, len(result))

C:\Users\Sayan\anaconda3\lib\site-packages\sklearn\metrics\\_classification.p y:1344: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero\_division` parameter to control this behavior.

\_warn\_prf(average, modifier, msg\_start, len(result))

```
In [95]: clf =SVC()
         clf.fit(X_train,y_train)
         accuracy=clf.score(X_test,y_test)
         print(accuracy*100)
         example=np.array([[4,2,1,1,1,2,3,2,5]])
         # print(example.shape)
         # print(example)
         # example=example.reshape(len(example),-1) #row to column vector
         # print(example.shape)
         # print(example)
         prediction=clf.predict(example)
         print(prediction)
         66.42857142857143
         [2]
In [ ]:
 In [ ]:
In [ ]:
 In [ ]:
```