```
In [95]: import sklearn
          from sklearn import datasets
          from sklearn import svm
          from sklearn.model selection import train test split
          from sklearn import metrics
 In [96]: | cancer = datasets.load_breast_cancer()
 In [97]: print(cancer.feature names)
           ['mean radius' 'mean texture' 'mean perimeter' 'mean area'
            'mean smoothness' 'mean compactness' 'mean concavity'
            'mean concave points' 'mean symmetry' 'mean fractal dimension'
            'radius error' 'texture error' 'perimeter error' 'area error'
            'smoothness error' 'compactness error' 'concavity error'
            'concave points error' 'symmetry error' 'fractal dimension error'
            'worst radius' 'worst texture' 'worst perimeter' 'worst area'
            'worst smoothness' 'worst compactness' 'worst concavity'
            'worst concave points' 'worst symmetry' 'worst fractal dimension']
 In [98]: print(cancer.target names)
          ['malignant' 'benign']
 In [99]: x = cancer.data
In [100]: x
Out[100]: 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-02],
                  [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]])
In [101]: | y = cancer.target
```

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In [102]: y
0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1,
                          0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0,
                1, 1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1,
                             1, 1, 0, 0, 0, 1, 0,
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                  1, 1, 1,
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                        0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1,
                             1, 1, 0, 0, 1, 0,
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                                              1,
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                          0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0, 0, 0, 1,
                0, 0, 1, 0,
                  1, 1, 0,
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                                              1,
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                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 1, 1,
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                                                1, 0, 1, 0, 1, 1, 1,
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                          1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1,
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                  0, 1, 1,
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                1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1])
In [103]: x_train, x_test, y_train, y_test = train_test_split(x,y,test_size=0.2)
In [104]: print(x_train.shape)
         (455, 30)
In [105]: |print(x_test.shape)
         print(y_train.shape)
         print(y test.shape)
         (114, 30)
         (455,)
         (114,)
In [106]: | classes = ['malignant', 'benign']
In [107]: | clf = svm.SVC()
         clf.fit(x_train, y_train)
Out[107]: SVC()
In [108]: |y_pred = clf.predict(x_test)
```

```
In [109]: | acc = metrics.accuracy_score(y_test,y_pred)
In [110]: print(acc)
          0.9035087719298246
In [111]: | clf1 = svm.SVC(kernel='poly')
          clf1.fit(x_train,y_train)
Out[111]: SVC(kernel='poly')
In [112]: y1_pred = clf1.predict(x_test)
In [114]: | acc1 = metrics.accuracy_score(y_test,y1_pred)
In [115]: print(acc1)
```