

In [36]:

#загружаем датасеты

```
from sklearn import datasets
breast_cancer = datasets.load_breast_cancer()
digits = datasets.load_digits()
```

In [37]:

#смотрим первый датасет

```
print breast_cancer.feature_names
print breast_cancer.data[0]
```

```
['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']
[ 1.79900000e+01  1.03800000e+01  1.22800000e+02  1.00100000e+03
  1.18400000e-01  2.77600000e-01  3.00100000e-01  1.47100000e-01
  2.41900000e-01  7.87100000e-02  1.09500000e+00  9.05300000e-01
  8.58900000e+00  1.53400000e+02  6.39900000e-03  4.90400000e-02
  5.37300000e-02  1.58700000e-02  3.00300000e-02  6.19300000e-03
  2.53800000e+01  1.73300000e+01  1.84600000e+02  2.01900000e+03
  1.62200000e-01  6.65600000e-01  7.11900000e-01  2.65400000e-01
  4.60100000e-01  1.18900000e-01]
```

In [38]:

#второй датасет

```
print digits.data[0]
```

```
[ 0.  0.  5. 13.  9.  1.  0.  0.  0.  0. 13. 15. 10. 15.  5.
  0.  0.  3. 15.  2.  0. 11.  8.  0.  0.  4. 12.  0.  0.  8.
  8.  0.  0.  5.  8.  0.  0.  9.  8.  0.  0.  4. 11.  0.  1.
 12.  7.  0.  0.  2. 14.  5. 10. 12.  0.  0.  0.  0.  6. 13.
 10.  0.  0.  0.]
```

In [39]:

```
from sklearn.naive_bayes import BernoulliNB, MultinomialNB, GaussianNB
from sklearn.model_selection import cross_val_score
```

In [40]:

```
print cross_val_score(BernoulliNB(), digits.data, digits.target).mean()
```

0.825823650778

In [41]:

```
print cross_val_score(MultinomialNB(), digits.data, digits.target).mean()
```

0.870877148974

In [42]:

```
print cross_val_score(GaussianNB(), digits.data, digits.target).mean()  
0.818600380355
```

In [43]:

```
print cross_val_score(BernoulliNB(), breast_cancer.data, breast_cancer.target).mean()  
0.627420402859
```

In [44]:

```
print cross_val_score(MultinomialNB(), breast_cancer.data, breast_cancer.target).mean()  
0.894579040193
```

In [45]:

```
print cross_val_score(GaussianNB(), breast_cancer.data, breast_cancer.target).mean()  
0.936749280609
```

In [46]:

```
#Выводы: 1) максимальное качество классификации на датасете breast_cancer: 0.937  
# 2) максимальное качество классификации на датасете digits: 0.871  
# 3) Из приведенных утверждений верны : C и D
```

In []: