**1.Missing Value Estimation**  
Gene expression data often contain missing expression values and it is very important to estimate those missing value as accurate as possible. This task of the project is to estimate missing value in the Microarray Data.

**input**: Gene expression data with missing vales (represented by **1.00E+99**)

**output:**A complete dataset with estimated values of missing data.

**2.Classification of Genes**   
Classification is to identify which of a set of categories a new observation belongs, on the basis of a training set of data. In the task , we have several different datasets with several sizes. For each dataset a training dataset, training label, and test dataset is provided. we use the training dataset and training label to build your classifier and predict the test label. The class label is represent by integer number.

Sample Data:

**Training data:**

1.1    2.1    2.1    5.2  
2.1    2.4    2.4    2.1  
3.1    1.5    2.6    1.5

**Training label**  
1  
1  
2

**Test data**

3.1    2.2    1.5    2.5  
2.1    2.1    2.1    2.6