Manual of the MPM-EDA.jar

The **MPM-EDA.jar** provides an implement of the **MPM-EDA agorithm**, and an implement of standrad **K-meams** as **benchmark**. Before using this jar package, please make sure the **JDK 7** has been correctly installed in your computer.

A simple demo is shown in the Fig. 1. This demo program will employ MPM-EDA algorithm on the yeast data set, and detailed results of the clustering will be printed.

```
System.setProperty("java.util.Arrays.useLegacyMergeSort", "true");

//The first parameter is the path of data set, the
//second is the index of the class tag(from 0 to n-1)
GeneralDataSet dataSet = new GeneralDataSet("yeast.data", 8);

//The second parameter is the initial distance(theta),
//the third one is a legacy parameter, it has no meaning and function now
MPMEDA mpm_eda = new MPMEDA(dataSet, 0.03, 1);

//This step starts to execute the MPM-EDA algorithm, the first parameter is
//the threshold(lamba), the second is the dimension of the data, except for the class tag dimension
Map<Integer, List<MetaCluster>> maptree = mpm_eda.launch_pro2(0.49, 8);

for(int i=1; i<maptree.keySet().size(); i++) {
    System.out.println("cluster num : " + maptree.get(i).size() + ", " +
            "error ratio : " + Evaluator.evaluateResu(maptree.get(i)));
}
```

Fig. 1

The format of your input data should be accordance with the data files we provide (iris, seeds and yeast. You can find the in the .rar file). **Notice** that if you run the algorithm on **seeds data set**, please remove the sentence of "*System.setProperty("java.util.Arrays.useLegacyMergeSort", "true");*"

To run the **K-means** algorithm, see the program shown in Fig. 2.

```
GeneralDataSet dataSet = new GeneralDataSet("yeast.data", 8);
//The second parameter is the number of clusters.
Kmeans kemans = new Kmeans(dataSet,10);

//The parameter '200' is the iteration
Map<Integer, List<MetaData>> resu = kemans.launch_pro(200);
System.out.println(Evaluator.evaluateResu(Evaluator.switcher(resu)));
```

Fig. 2

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