Manual of use

BiMine+ is an algorithm that discovers biclusters in microarray data. It is implemented in Java programming language. The BiMine+ software is free of charge for academic use.

BiMine+ is an improved version of BiMine.

The BiMine+ program command should be the following format:

```
BiMine+.jar InputFile.txt δ β OutputFile.txt
```

where:

- InputFile.txt is the microarray dataset. Each line must contain only gene name with their expression values. The condition names must be removed (see Input File Format). Missing values are replaced by random ones.

- δ is the threshold of minimum number of conditions.

- β is the threshold of the Average Spearman's Rho (ASR $\in$ [-1..1]).

- OutputFile.txt is the result file. Each line contains one bicluster. One bicluster contains a subset of genes, a subset of conditions and the ASR value. The conditions are considered as a number. In fact, the conditions numbering start from 0, e.g., the first condition in the InputFile is transformed in the OutputFile to 0, the second condition to 1, etc.

The BiMine+.jar and the InputFile.txt must be in the same directory. The OutputFile is created in the same directory.

Input File Format:

An input file should be a space or tab-delimited text file. The first column should contain gene names. And the first row of the condition names must be removed.

An example input file should look like:

$gene_0$	108	...	-46.98
$gene_i$	...	...	...
$gene_n$	34.6	-466	0.87