

BicFinder: A Biclustering Algorithm for Microarray Data Analysis

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

The BicFinder program command should be the following format:

BicFinder.jar InputFile.txt ACSI ASR 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 values.
- ACSI is the threshold of the average correspondence similarity index ($ACSI \in [0..1]$).
- ASR 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 ASR value.

The BicFinder.jar and the InputFile.txt must be 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. An example input file should look like:

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