BicFinder: a biclustering algorithm for microarray data analysis

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Résumé en anglais	In the context of microarray data analysis, biclustering allows the simultaneous identification of a maximum group of genes that show highly correlated expression patterns through a maximum group of experimental conditions (samples). This paper introduces a heuristic algorithm called BicFinder (The BicFinder software is available at: http://www.info.univ-angers.fr/pub/hao/BicFinder.html [11]) for extracting biclusters from microarray data. BicFinder relies on a new evaluation function called Average Correspondence Similarity Index (ACSI) to assess the coherence of a given bicluster and utilizes a directed acyclic graph to construct its biclusters. The performance of BicFinder is evaluated on synthetic and three DNA microarray datasets. We test the biological significance using a gene annotation web-tool to show that our proposed algorithm is able to produce biologically relevant biclusters. Experimental results show that BicFinder is able to identify coherent and overlapping biclusters.
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