

BiMine+: An efficient algorithm for discovering relevant biclusters of DNA microarray data

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| R sum  en anglais | <p>Biclustering is a very useful tool for analyzing microarray data. It aims to identify maximal groups of genes which are coherent with maximal groups of conditions. In this paper, we propose a biclustering algorithm, called BiMine+, which is able to detect significant biclusters from gene expression data. The proposed algorithm is based on two original features. First, BiMine+ is based on the use of a new tree structure, called Modified Bicluster Enumeration Tree (MBET), on which biclusters are represented by the profile shapes of genes. Second, BiMine+ uses a pruning rule to avoid both trivial biclusters and combinatorial explosion of the search tree. The performance of BiMine+ is assessed on both synthetic and real DNA microarray datasets. Experimental results show that BiMine+ competes favorably with several state-of-the-art biclustering algorithms and is able to extract functionally enriched and biologically relevant biclusters.</p> |
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