Abstract

Biclustering algorithms perform simultaneous row and column clustering of a given data matrix. In gene expression dataset a bicluster is a subset of genes that exhibit similar expression patterns through a subset of conditions. Biclustering is a useful data mining technique for identifying local patterns from gene expression data. In this paper biclusters are identified in two steps. In the first step high quality bicluster seeds are generated using K-Means clustering algorithm. These seeds are then enlarged using Cardinality based Greedy Randomized Adaptive Search Procedure (CGRASP) which is a multi-start metaheuristic method in which there are two phases, construction and local search. The Experimental results on the benchmark datasets prove that CGRASP is capable of identifying biclusters of high quality compared to many of the already existing biclustering algorithms. Moreover far better biclusters are obtained in this algorithm compared to the already existing algorithm based on the same GRASP metaheuristics.

Reference

Application of Cardinality based GRASP to the Biclustering of Gene Expression Data

- Federico Divina and Jesus S. Aguilar-Ruize, "Biclustering of Expression Data with Evolutionary computation", IEEE Transactions on Knowledge and Data Engineering, 2006. Vol. 18, pp. 590-602.

Index Terms

Computer Science

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Application of Cardinality based GRASP to the Biclustering of Gene Expression Data

Key words

Network Security

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