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Incorporating gene ontology information in gene expression data clustering using multiobjective evolutionary optimization: application in yeast cell cycle data. (English)

Zbl 1409.92167

Summary: The advances in microarray technology have allowed the biologists to simultaneously study the levels of expression of a large set of genes over different time points. Clustering algorithms are used to discover groups of genes that are similarly expressed over all the experimental conditions. In this chapter, an approach for combining experimental gene expression information and biological information in the form of Gene Ontology (GO) knowledge through multiobjective clustering has been presented. The proposed method combines the expression-based and GO-based measures to compute the distances between the genes. Moreover, it simultaneously optimizes two objective functions, one from gene expression point of view and another from GO point of view. The performance of the proposed technique has been demonstrated on real-life gene expression dataset of yeast cell cycle. Moreover, biological relevance studies have been conducted for the produced clusters to demonstrate the effectiveness of the proposed technique.

For the entire collection see [Zbl 1401.90021].

MSC:
92D10 Genetics and epigenetics
62H30 Classification and discrimination; cluster analysis (statistical aspects)
68T20 Problem solving in the context of artificial intelligence (heuristics, search strategies, etc.)
68T30 Knowledge representation
90C29 Multi-objective and goal programming
92C37 Cell biology

Keywords:
microarray gene expression; genetic algorithms; multiobjective clustering; gene ontology; semantic similarity; yeast cell cycle

Software:
KEGG; EXPANDER ; SPEA2

Full Text: DOI

References:


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