Abstract

Microarrays are made it possible to simultaneously monitor the expression profiles of thousands of genes under various experimental conditions. Identification of co-expressed genes
Effective Clustering Algorithms for Gene Expression Data

and coherent patterns is the central goal in microarray or gene expression data analysis and is an important task in Bioinformatics research. In this paper, K-Means algorithm hybridised with Cluster Centre Initialization Algorithm (CCIA) is proposed Gene Expression Data. The proposed algorithm overcomes the drawbacks of specifying the number of clusters in the K-Means methods. Experimental analysis shows that the proposed method performs well on gene Expression Data when compare with the traditional K-Means clustering and Silhouette Coefficients cluster measure.

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