

Finding Bicluster on Gene Expression Data of Lymphoma Based on Singular Value Decomposition and Hierarchical Clustering

Authors : Alhadi Bustaman, Soeganda Formalidin, Titin Siswantining

Abstract : DNA microarray technology is used to analyze thousand gene expression data simultaneously and a very important task for drug development and test, function annotation, and cancer diagnosis. Various clustering methods have been used for analyzing gene expression data. However, when analyzing very large and heterogeneous collections of gene expression data, conventional clustering methods often cannot produce a satisfactory solution. Biclustering algorithm has been used as an alternative approach to identifying structures from gene expression data. In this paper, we introduce a transform technique based on singular value decomposition to identify normalized matrix of gene expression data followed by Mixed-Clustering algorithm and the Lift algorithm, inspired in the node-deletion and node-addition phases proposed by Cheng and Church based on Agglomerative Hierarchical Clustering (AHC). Experimental study on standard datasets demonstrated the effectiveness of the algorithm in gene expression data.

Keywords : agglomerative hierarchical clustering (AHC), biclustering, gene expression data, lymphoma, singular value decomposition (SVD)

Conference Title : ICPMS 2017 : International Conference on Port and Maritime Security

Conference Location : Bali, Indonesia

Conference Dates : October 23-24, 2017